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Minimum DB seq
Maximum DB seq
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-Q
-Q
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-None-frame+ p2n.model -DEV=xlh
-Q
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-Q
-NINMATCH=0.1
-Q
-NINMATCH=0.1
-DB=PublIshed Applications NA -QFMT=fastap -SUPFTX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bite -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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length: 2000000000
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                              /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	ö	tch	Length	DB	ID	cription
1	1599	100.0	1101	19	US-10-659-004-103	Sequence 103, App
2	59.	5	25	18	S-10-764-604-28	equence 28, 1
w	59.	'n	74	15	-10-171-581-17	equence 170, Ap
4.	359.	<u>ب</u>	74	15	-10-177-293-26	equence 263, Ap
Ŋ	59.	ŗ	74	17	-10-172-118-140	equence 1400, A
6	359.	85.0	4	17	S-10-342-887-14	equence 1400, A
7	359.	ņ	74		S-10-769-612-1	equence 1, Appl
æ	359.	<u>ب</u>	55	18	-10-357-930-	equence 25736,
	359.	'n	53	14	-10-198-846-1000	equence 10007
10	356.	4.	2268	17	S-10-188-832-	equence 176,
11	356.	4.	26	19	8-10-659-004-10	nce 105,
12		4	46	17	-10-295-027-	equence 55,
13	356.	4	46		-10-295-027-83	equence 838,
14	•	٠.	46		-10-295-027-	equence 878,
15	356.	4.	46	17	-10-058-270A-2	equence 29,
16	; 6	84.8	3609	19	-10-855-588-21	equence 21,
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19		4	3445		10-044-564-2	equence 25,
20	352.	4	44	19	-10-659-004-9	equence 97, 1
21	351.	4.	31		-10-659-004-1	equence 107,
22	349.		77	17	-10-182-033-3	e u
23	347.	4	44	19	-10-659-004-	equence 113,
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29	100	63.0	81	19	S-10-855-588-23	equence 23,
30	87	.4	59	17	S-10-131-410-1	equence 12,
31	831	٠.	Çī	17	-10-182-033-1	equence 12, App
32	718	.4	30	18	S-10-357-930-2326	equence 23267,
u	نسر	44.9	30	18	8-10-357-930-2	equence 29142,
34	<u>, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,</u>	4.	4	10	-09-814-353-2202	equence 22020,
, W		4.	N	6	S-10-269-909-39	equence 39,
2 0	710		3 6	۰ ۱	5-10-789-E61-1	Sequence 410
י פ	710	٠.	u L	٠,	10-883-016-1	mience 14,
	ũ,	44.9	4	18	-10-322-696-5	equence 5
40	712	4	29	18	-10-723-860-	equence 8029, A
41	712	4.	74	18	-10-322-696-2	equence 2, Appl
42	7	რ	91	19	-10-659-004	equence 99,
43	514.5	32.2	366	10	95	equence 30283
44	439	7.	4573	છ	09-880-107	quence 164
	439	7	7	10	US-09-960-706-489	e 489,

ALIGNMENTS

US-10-659-004-103

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Sequence 103, Application US/10659004
Publication No. US20050048507A1
GENERAL INFORMATION:
APPLICANY: Zhong et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD:
FILE REFERENCE: 21402-608
CURRENT APPLICATION NUMBER: US/10/659,004
CURRENT FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: 60/295,607
PRIOR TILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/295,661
PRIOR APPLICATION NUMBER: 60/295,404
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,418
PRIOR APPLICATION NUMBER: 60/296,418
PRIOR APPLICATION NUMBER: 60/297,414
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/297,414
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/297,414
PRIOR FILING DATE: 2001-06-01
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EENGTH: 1101
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (123)..(1028)
US-10-659-004-103
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PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-14
PRIOR REPLICATION NUMBER: 60/298,556
PRIOR RELING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/299,949
PRIOR APPLICATION NUMBER: 60/299,949
PRIOR FILING DATE: 2001-06-21
PRIOR PRIOR DATE: 2001-06-21
PRIOR PRIOR DATE: 2001-06-26
Remaining Prior Application data removed - 5
NUMBER OF SEQ ID NOS: 187
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 103
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ValLysGlnAlaValLeuTyrAsnAlaLeuSerAlaMetLeuAlaTyrLeuGlyMetAla
                                                  CysHisGluLeuProHisGluLeuGlyAspPheAlaValLeuLeuLysAlaGlyMetThr
                                                                                          ATTGGTGCTGTTTACTGAAGGCTTATCAAGTGGTTTAAGTACTTCTGTTGCTGTTTC
                                                                                                            IleGlyAlaAlaPheThrGluGlyLeuSerSerGlyLeuSerThrSerValAlaValPhe
                                                                                                                                                        ACTITIGGCCTGGATGGTGATAATGGGTGATGGCCTGCACAATTTCAGCGATGGTCTAGCA
                                                                                                                                                                        ThrLeuAlaTrpMetValIleMetGlyAspGlyLeuHisAsnPheSerAspGlyLeuAla
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GENERAL INFORMATION:
APPLICANT: McLachlan, Karen
APPLICANT: Glaser, Scott
APPLICANT: Glaser, Scott
APPLICANT: Peach, Robert
INFORMATION: Compositions and Methods
TITLE OF INVENTION: LIV-1
FILE REFERENCE: 2159,0030001
CURRENT APPLICATION NUMBER: US/10/764,604
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US 60/442,535
PRIOR FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
INVERTAL 7356
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-764-604-28
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No.:
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                                                                                                                                                                               1 MetAlaArgLy8LeuSerVallleLeuIleLeuThrPheAlaLeuSerValThrAsnPro
                                                   AlaSerAspHisGlyCysSerArgTrpGlyTyrPhePheLeuGlnAsnAlaGlyMetLeu
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              PheTyrArgTyrGlyGluAsnAsnSerLeuSerValGluGlyPheArgLysLeuLeuGln
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TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia FILE REFERENCE: 9301-157-999	gyue , Peter	ion No. US20030104426A1 INFORMATION:	RESULT 3 US-10-171-581-170 : Sequence 170. Application US/10171581	AAAATC	294 HistysileValpheArglleAsnphe 302	7 174 LeuGlnAsnAlaGlyMetLeuLeuGlyPheGlyIleMetLeuLeuIleSerIlePheGlu 293	254 PROGLUMECLEUHIBHSHABDALASELABDHIBGLYCYBSELAEGIDGLYTYTTETTE 2/3	234 met it piternekateelinikatediybeeteenethis valkatateevalkaspeet val 	1981 CTGGCGTATCTTGGAATGGCCAACAGGAATTTTCATTGGTCATTATGCTGAAAATGTTTCT	191 CTACTAAAGGCTGGCATGACCGTTAAGCAGGCTGTCCTTTATAATGCATTGTCAGCCATG	174 SertinfServalAlaValEneCysHisGluceProdisGluceUGL/AsppineAlaVal	154 AsnPheSerAspGlyLeuAlaIleGlyAlaAlaPheThrGluGlyLeuSerSerGlyLeu	134 LeuLysAspalaGlyValAlaThrLeuAlaTrpMetValIlaMetGlyAspGlyLeuHis	120HisHisProHisSerHisSerGlnArgTyrSerArgGluGlu 133	L L	1561 GTCTACAATGAATATGTACCCCAGAGGGTGCAAGAATAAATGCCATTCCACATTTCCACGAT 1620	1501 CAGCAGCCTGCAGTCTTGGAAGAAGAAGATCATGATAGCTCATGCTCACAGGAA 1560	1191111AUGANGUANALIGANGGANALIGANGANGKANGANGKANGKANGKANGKANGKANGKANGKA	1381 AAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAATGAGGAGAAAGTAGATACA 119

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110	Db 618 CACCGACCAGAACATGCCAGTGGTAGAAGGAATGTCAAGGACAGTGTTAGTGCTAGTGAA 677
1698 GTCTACAATGAATATGTACCCAGAGGGGGGGGAAGAATAAATGCCATTCACATTTCCACGAT	Qy 119 119
119	Db 558 CCAGACCATGACTCAGATAGTTCAGGTAAAGATCCTAGAAACAGCCAGGGGAAAGGAGCT 617
Db 1638 CAGCAGCCTGCAGTCTTGGAAGAAGAAGAGGTCATGATAGCTCATGCTCATCCACAGGAA 1697	Qy 119 119
	Db 498 GAGCATCACTCTGACCATAATCATGCTGCTTCTGGTAAAAATAAGCGAAAAAGCTCTTTGC 557
1578 GATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAGCCCTCCCCACTTTGATTCT	Qy 119 119
Oy 119 119	Db 438 GACCACGAGCATCACTCAGACCATGAGCCTCAGACCATGAGCATCACTCAGACCAC 497
Db 1518 AAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAATGAGGAGAAAGTAGATACA 1577	Qy 101 AapHisGluHisHisSerAspHisGluArgHisSerAspHisGluHisHisSerAsp 119
Qy 119 119	3/0 MITHINGCNIANTHANNITANNATONITANANATONITANANATONIVANANATONITANA
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Db 1398 GCTCTAGGAGGCCTGTATTTCATGTTCTTGTTGAACATGTCCTCACATTGATCAAACAA 1457	TICTACCGCTATGGAGAAAATAATTCTTTGTCAGTTGAAGGGTTCAGAAAAATTACTTCAA
Qy 119 119	61 PheTyrardTyrGlyGlijagnAgnSerLeuSerValGljjGlyDheArdLygLeuCln
Db 1338 CTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCCACGTGGAAGGGTCTAACA 1397	258 GAATCTGGCATTAATGTTGACTTGGCAATTTCCACACGGCAATATCATCTACAACAGCTT
Qy 119 119	41 GluSerGlvIleAsnValAspLeuAlaIleSerThrArqGlnTvrHisLeuGlnGlnLeu
Db 1278 CATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGAGGACCACTTTTCAGTCAT 1337	198 CTTCATGAACTAAAAGCAGCTGCTTTCCCCCCAGACCGAGAAAATTAGTCCGAATTG
1199	Qy 21 LeuHisGluLeuLysAlaAlaAlaPheProGlnThrThrGluLysIleSerProAsnTrp 40
1218 GGGACTTTGAGTGGTGATGCTTTTTTACACCTTCTTCCACATTCTCATGCAAGTCACCAC	138 ATGGCGAGGAAGTTATCTGTAATCTTGATCCTGACCTTTGCCCTCTCTCT
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Db 1158 CCTCTCATGAATCGGGTGTTTTTCAAATTTCTCCTGAGTTTCCTTGTGGCACTGGCCGTT 1217	i-104 (1-302) x US-10-171-5
	85.02% Indels:
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Qy 119 119	1.31e-150
Db 1038 ACAAGTGAAAAGAAGGCTGAAATCCCTCCAAAGACCTATTCATTACAAATAGCCTGGGTT 1097	Alignment Scores:
119	; DATABASE ENTRY DATE: 2001-06-18 US-10-171-581-170
TTCAACTATCTCTGTCCAGCCATCATCAACCAAATTGATGCTAGATCTTGTCTGATTCAT	; PUBLICATION INFORMATION: ; DATABASE ACCESSION NUMBER: U41060
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Db 858 CCCCGAAAAGGCTTTATGTATTCCAGAAACACAAATGAAAATCCTCAGGAGTGTTTCAAT 917	; CURRENT APPLICATION NUMBER: US/10/171,581 ; CURRENT FILING DATE: 2002-06-14
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APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION NUMBER: US/10/177,293
CURRENT APPLICATION NUMBER: US/01/29,887
PRIOR APPLICATION NUMBER: US/01/29,887
PRIOR APPLICATION NUMBER: US/0301,572
PRIOR APPLICATION NUMBER: US/0301,572
PRIOR APPLICATION NUMBER: US/0306,501
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-09-16
PRIOR APPLICATION NUMBER: US/03/36,501
PRIOR APPLICATION NUMBER: US/03/36,502
PRIOR APPLICATION NUMBER: US/03/36,585
PRIOR APPLICATION NUMBER: US/03/362,585
PRIOR APPLICATION NUMBER: US/03/3
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Hortobagyi, Gabriel
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Monahan, John
Meyers, Rachel E.
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Wang, Youzhen
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Kamatkar, Shubhangi
Mertens, Maureen
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Zhao, Xumei
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; TYPE: DNA
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US-10-177-293-263
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Db 258 GAATCTGGCATTAATGTTGACTTGGCAATTTCCACACGGCAATATCATCTACAACAGCTT 317 Qy 61 PheTyrArgTyrGlyGluAsnAsnSerLeuSerValGluGlyPheArgLysLeuLeuGln 80	GluSerGlyI1eAsnValAspLeuAlaI1eSerThrArgGlnTyrHisLeuGlnGlnLeu	Qy 21 LeuHisGluLeuLysAlaAlaAlaAheProGlnThrThrGluLysIleSerProAsnTrp 40	Db 138 ATGGCGAGGAAGTTATCTGTAATCTTGATCCTGACCTTTTGCCCTCTCTGTCACAAATCCC 197	US-10-659-004-104 (1-302) x US-10-172-118-1400 (1-2744) Qy 1 MetAlaArgLysLeuSerValIleLeuIleLeuThrPheAlaLeuSerValThrAsnPro 20	## ## ## ### ### #####################	1359.50 Matches: milarity: 40.32% Conservative: cimilarity: 40.108 Mismarches:		US-10-172-118-1400	; DATABASE ENTRY DATE: 2001-06-T8	ORGANISM: Homo sapiens DIBLICATION INCORMATION.	LEASTH: 2744	NUMBER OF SEQ ID NOS: 2699	PRIOR EPILICATION NUMBER: 60/380,770 PRIOR ETILING DATE: 2002-05-14	CURRENT APPLICATION NUMBER: US/10/172,118	FILE REFERENCE: 9301-175-999	, APPLICANT: Van de Vijver, Marc APPLICANT: Van de Vijver, Marc	; APPLICANT: Roberts, Chris	APPLICANT: Line, rucchy APPLICANT: Line, Peter APPLICANT: Mac Mac		Publication No. US203030224374A1 GENERAL TURORBARTION	US-102: US-102			294 Historalleval Dhearcalleagaphe 302	TACAGAATGCTTGGGTTTTGGAATTATGTTACTTATTTCCATATTTGAA	274 LenGlnAsnAlaGlvMetLeuLeuGlvPheGlvIleMetLeuLeuIleSerIlePheGlu	2238 CCTGAAATGCTGCAAAATGCTAGTGACGATGGACCGCTGGGGGGTATTTTTTTT	254 ProGluMetLeuHisAsnAspAlaSerAspHisGlvCvsSerArgTrpGlvTvrPhePhe	2178 ATCHCGATATTTCCACTTTACTCCTCGCCTTATTCATGTATGTTGCTCTCGGTTGATATGGTA	234 MetTrpIlePheAlaLeuThrAlaGlyLeuPheMetHisValAlaLeuValAspMetVal	TIGGCGTATCTTGGAATGGCAACAGGAATTTTCATTGGTCATTATGCTGAAAATGTTTCT	214

; GENERAL INFORMATION: ; GENERAL INFORMATION: APPLICANT: DAI, Hongyu
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Sequence 1, Application US/10769612

Publication No.-US20040141983A1

GENERAL INFORMATION:

APPLICANT: Law, Debbie
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Murray, Richard
APPLICANT: Sound Compositions Against Cancer Antigen LIV-1 And
FILE REFERENCE: 05882-0129-01908

FULL REFERENCE: 05882-0129-012

FULL REFERENCE: 09882-0129-012

FULL REFERENCE: 099642,034

FILE REFERENCE: 2000-08-18

PRIOR APPLICATION NUMBER: 099642,034

PRIOR APPLICATION NUMBER: 099642,034

PRIOR APPLICATION NUMBER: 09963,137

PRIOR APPLICATION NUMBER: 099453,137

PRIOR APPLICATION NUMBER: 099453,137

PRIOR APPLICATION NUMBER: 09968,865

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetTrpIlePheAlaLeuThrAlaGlyLeuPheMetHisValAlaLeuValAspMetVal
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               ACAAGTGAAAAGAAGGCTGAAATCCCTCCAAAGACCTATTCATTACAAATAGCCTGGGTT 109:
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                                                                                                                                 GCATCAAAGCTACTGACATCTCATGGCATGGGCATCCAGGTTCCGCTGAATGCAACAGAG 977
                                                                                                                                                                                           CCCCGAAAAGGCTTTATGTATTCCAGAAACACAAATGAAAATCCTCAGGAGTGTTTCAAT 917
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1098	GGTGGTTTTATAGCCATTTCCATCATCAGTTTCCTGTCTCTGCTGGGGGTTATCTTAGTG 1	157
. 119	1	.19
1158	CCTCTCATGAATCGGGTGTTTTTCAAATTTCTCCTGAGTTTCCCTTGTGGCACTGGCCGTT 1	1217
119	1	.19
1218	GGGACTTTGAGTGGTGATGCTTTTTTACACCTTCTTCCACATTCTCATGCAAGTCACCAC 1	.277
119		.19
1278	CATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGAGGACCACTTTTCAGTCAT 1	.337
119	1	.19
1338	CTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCCACGTGGAAGGGTCTAACA 1	397
119	1	
1398	GCTCTAGGAGGCCTGTATTTCATGTTTCTTGTTGAACATGTCCTCACATTGATCAAACAA 1	1457
119		119
1458	TTTAAAGATAAGAAGAAAAGAATCAGAAGAAACCTGAAAATGATGATGATGTGGAGATT 1	LS17
119	1	119
1518	AAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAATGAGGAGAAAGTAGATACA 1	1577
119		119
1578	GATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAGCCCCTCCCACTTTGATTCT 1	1637
119	1	119
1638	CAGCAGCCTGCAGTCTTGGAAGAAGAAGAGGTCATGATAGCTCATGCTCATCCACAGGAA 1	1697
119		119
1698	GTCTACAATGAATATGTACCCAGAGGGTGCAAGAATAAATGCCATTCACATTTCCACGAT	1757
119		119
1758	CCAT	1817
120	HisHisProHisSerHisSerGlnArgTyrSerArgGluGlu	133
1818	GGAG	1877
134	LeuLysAspAlaGlyValAlaThrLeuAlaTrpMetValIleMetGlyAspGlyLeuHis	153 1937
154 1938		173 1997
174 1998	SerThr8erValAlaValPheCysHisGluLeuProHisGluLeuGlyAspPheAlaVal	193 2057
194 2058	LeuLeuLysAlaGlyMetThrValLysGlnAlaValLeuTyrAsnAlaLeuSerAlaMet 	213 2117
214	LeuAlaTyrLeuGlyMetAlaThrGlyIlePheIleGlyHisTyrAlaGluAsnValSer 	233
23	etTrpIlePheAlaLeuThrAlaGlyLeuPheMetHisValAlaLeuValAspMetVal	253

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; IOCATION: 1, 2, 3506, 3507, 3508, 3509, 3510, 3511, 3512, 3513,
; IOCATION: 3515, 3516, 3517, 3518, 3519, 3520, 3521, 3522, 3523
; OTHER INFORMATION: n = A,T,C or G
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TYPE: DNA
ORGANISM: Homo sapiens
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CTTCATGAACTAAAAGCAGCTGCTTTCCCCCCAGACCACTGAGAAAATTAGTCCGAATTGG
          LeuHisGluLeuLysAlaAlaAlaPheProGlnThrThrGluLysIleSerProAsnTrp
                                      ATGGCGAGGAAGTTATCTGTAATCTTGATCCTGACCTTTGCCCCTCTCTGTCACAAATCCC
                                                  MetAlaArgLysLeuSerValIleLeuIleLeuThrPheAlaLeuSerValThrAsnPro
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RESULT 9	Qy 294 HisLysIleValPheArgIleAsnPhe 302	2298 TTACAGAATGCTGGGATGCTTTTGGGT	274 LeuGlnAsnAlaGlyMetLeuLeuGlyPheGlyIleMetLeuLeuIleSerIlePheGlu	Qy 254 ProGluMetLeuHisaanAapAlaSerAapHisGlyCysSerArgTrpGlyTyrbhePhe 273	2178 ATGTGGATATTTGCACTTACTGCTGGCTTATTCATGTATGT	234 MetTrpllePheAlaLeuThrAlaGlyLeuPheMetHisValAlaLeuValAspMetVal	Qy 214 LeuAlaTyrLeuGlyMetAlaThrGlyIlePheIleGlyHisTyrAlaGluAsnValSer 233	THE TAKE THE PROPERTY OF THE P	1998	174 SerThrSerValAlaValPheCysHisGluLeuProHisGluLeuGlyAspPheAlaVal	AATTTCAGCGATGGCCTAGCAATTGGTGCTGCTTTTACTGAAGGCTTATCAAGTGGTTTA	154 landhagarlandivianilalladivlalalladhaThrGlnGlvianSerSerGlvian	Qy 134 LeuLysAspAlaGlyValAlaThrLeuAlaTrpMetValIleMetGlyAspGlyLeuHis 153	1818 CATCACCACCACAAAACCATCCTCACAGTCACAGCCAGCGCTACTCTCGGGAGGAG	Db 1758 ACACTCGGCCAGTCAGACGATCTCATTCACCACCATCATGACTACCATCATATTCTCCCAT 1817 Ov 120HisHisProHisSerHisSerGlnArgTvrSerAraGluGlu 133	119	Db 1698 GTCTACAATGAATATGTACCCAGAGGGTGCAAGAATAAATGCCATTCACATTTCCACGAT 1757	Qy 119 119	Db 1638 CAGCAGCCTGCAGTCTTGGAAGAAGAAGAGGTCATGATAGCTCATGCTCATCCACAGGAA 1697	119.	Db 1578 GATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAGCCCTCCCACTTTGATTCT 1637	1518 AAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAATGAGGAGAAAGTAGATACA	Оу 119 119	Db 1458 TTTAAAGATAAGAAAAAAAAAGAATCAGAAGAAACCTGAAAATGATGATGATGTGGAGATT 1517	Oy 119 119	Db 1398 GCTCTAGGAGGCCTGTATTTCATGTTTCTTGTTGAACATGTCCTCACATTGATCAAACAA 1457	Qy 119 119	Db 1338 CTGTCTTCTCAAAACATAGAAGGAAAGTGCCTATTTTGATTCCACGTGGAAGGGTCTAACA 1397	Qy 119 119

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APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Aziz, Natasha

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions

TITLE OF INVENTION: Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: Cancer

FILE REFERENCE: 018501-002330US

CURRENT APPLICATION NUMBER: US/10/188,832

CURRENT FILING DATE: 2002-11-22

PRIOR APPLICATION NUMBER: US 60/302,814

PRIOR FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: US 60/310,099

PRIOR APPLICATION NUMBER: US 60/310,099

PRIOR APPLICATION NUMBER: US 60/310,099

PRIOR APPLICATION NUMBER: US 60/313,705

PRIOR APPLICATION NUMBER: US 60/343,705

PRIOR FILING DATE: 2001-11-08

PRIOR FILING DATE: 2001-11-08

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PRIOR FILING DATE: 2001-07-03

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27	8 AsnAlaLeuSerAlaMetLeuAlaTyrLeuGlyMetAlaThrGlyIlePheIleGlyHis 2	20
07 980	8 LeuGlyAspPheAlaValLeuLeuLysAlaGlyMetThrValLysGlnAlaValLeuTyr 2	18 192
87 920	8 GlyLeuSerSerGlyLeuSerThrSerValAlaValPheCysHisGluLeuProHisGlu 1	16: 186:
67 860	MetGlyAspGlyLeuHisAsnPheSerAspGlyLeuAlaIleGlyAlaAlaPheThrGlu 1	148 1801
47 800	ArgTyrSerArgGluGluLeuLysAspAlaGlyValAlaThrLeuAlaTrpMetValIle 1	128 1741
27 740	TACCATCATATTCTCCATCATCACCACCACCACCAAAACCACC	120 1681
680	CATTCACATTTCCACGATACACTCGGCCAGTCAGACGATCTCATTCACCACCATCATGAC 1	1621
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620	1 CATGCTCATCCACAGGAAGTCTACAATGAATATGTACCCAGAGGGTGCAAGAATAAATGC	156:
19] 11	119
560	L CCCTCCCACTTTGATTCTCAGCAGCCTGCAGTCTTGGAAGAAGAAGAGAGGTCATGATAGCT 15	1501
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500	L GAGGAGAAAGTAGATACAGATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAG 15	1441
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140	L GATGATGATGTGGAGATTAAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAAT 14	1381
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380	. СТСАСАТТGАТСАААСААТТТАААGАТААGААGААААAGAATCAGAAGAAACCTGAAAAT 13	1321
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320	ACGTGGAAGGGTCTAACAGCTCTAGGAGGCCTGTATTTCATGTTTCTTGTTGAACATGTC 1	1261
61	11	119
260	GGACCACTTTTCAGTCATCTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCC 12	1201
6) 11	119
200	. TCTCATGCAAGTCACCACCATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGA 12	1141
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40	. CTTGTGGCACTGGCCGTTGGGACTTTGAGTGGTGATGCTTTTTTTACACCTTCTTCCACAT 11	1081
9	11	119
)80	. CTGGGGGTTATCTTAGTGCCTCTCATGAATCGGGTGTTTTTCAAATTTCTCCTGAGTTTC 10	1021
19) 11	119
)20	TTACAAATAGCCTGGGTTGGTGGTTTTATAGCCATTTCCATCAGCATTCCTGTCTCTG 10	961
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0	. AGATCTTGTCTGATTCATACAAGTGAAAAGAAGGCTGAAATCCCTCCAAAGACCTATTCA 96	901
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PRIOR APPLICATION NUMBER: 08/295,607
PRIOR APPLICATION NUMBER: 60/295,607
PRIOR TILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR FILING DATE: 2001-06-04
PRIOR PRILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR APPLICATION NUMBER: 60/296,418
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: CuraSe; SEQ ID NO 105; LENGTH: 2268; TYPE: DNA; ORGANISM: Homo
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PRIOR FILLING DATE: 2001-06-11
PRIOR PELLING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/297,567
PRIOR APPLICATION NUMBER: 60/298,285
PRIOR APPLICATION NUMBER: 60/298,285
PRIOR APPLICATION NUMBER: 60/298,556
PRIOR APPLICATION NUMBER: 60/299,949
PRIOR APPLICATION NUMBER: 60/299,949
PRIOR APPLICATION NUMBER: 60/300,883
PRIOR FILING DATE: 2001-06-26
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                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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MetAlaArgLysLeuSerVallleLeuIleLeuThrPheAlaLeuSerValThrAsnPro
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1338 GGACCACTTTTCAGTCATCTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCC 1397	- Db	Qy 41 GluSerGlyIleAsnValAspLeuAlaIleSerThrArgGlnTyrHisLeuGlnGlnLeu 60
119	φ	Db 198 CTTCATGAACTAAAAGCAGCTGCTTTCCCCCAGACCACTGAGAAAATTAGTCCGAATTGG 257
1278 TCTCATGCAAGTCACCACCATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGA	Db	laAlaAlaPheProGlnThrThrGluLyBileSerProAsnTip 4
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1218 CTTGTGGCACTGGCCGTTGGGACTTTGAGTGGTGATGCTTTTTTACACCTTCTTCCACAT 1277	da	1 MetAlaArgLysLeuSerVallIeLeuIILeLeuInrhealaLeuSerValIIILSII-IO
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1158 CTGGGGGTTATCTTAGTGCCTCTCATGAATCGGGTGTTTTTCAAATTTCTCCTGAGTTTC	дь	Galba:
119	Q	ry Match: 39.8/6 Fitshidaceries: RY Match: 84.83% Indels: Cana.
1098 TTACAAATAGCCTGGGTTGGTGGTTTTATAGCCATTTCCATCATCAGTTTCCTGTCTCTG	Db	1356.50 lmilarity: 40.00%
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1038 AGATCTTGTCTGATTCATACAAGTGAAAAGAAGGCTGAAATCCCTCCAAAGACCTATTCA 1097	ф	US-10-295-027-55
	γQ	
978 CCGCTGAATGCAACAGAGTTCAACTATCTCTGTCCAGCCATCATCAACCAAATTGATGCT 1037	ממ	SEQ ID N
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918 CCTCAGGAGTGTTTCAATGCATCAAAGCTACTGACATCTCATGGCATGGGCATCCAGGTT 977	מם	
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858 AATGAATCTGTGAGTGAGCCCCGAAAAGGCTTTATGTATTCCAGAAACACAAATGAAAAT	dd	PRIOR PRIOR
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798 TCCACTCCACCCAGTGTCACATCAAAGAGCCGGGTGAGCCGGCTGGCT	מם	PRIOR PRIOR
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738 TTTCTAGAGACAATAGAGACTCCAAGACCTGGAAAACTCTTCCCCAAAGATGTAAGCAGC	DЬ	PRIOR
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678 AGTGTTAGTGCTAGTGAAGTGACCTCAACTGTGTACAACACTGTCTCTGAAGGAACTCAC	Db	PRIOR
119	Q	PRIOR PRIOR
618 AGCCAGGGAAAGGAGCTCACCGACCAGAACATGCCAGTGGTAGAAGGAATGTCAAGGAC	Dъ	; CURRENT FILING DATE: 2002-11-13 ; PRIOR APPLICATION NUMBER: US 09/663,733
119	Q	; FILE REFERENCE: 018501-012500US ; CURRENT APPLICATION NUMBER: US/10/295,027
558 AAGCGAAAAGCTCTTTGCCCAGACCATGACTCAGATAGTTCAGGTAAAGATCCTAGAAAC	ФФ	; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and ; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
119	Qy	APPLICANT: Watson, Susan R. APPLICANT: Eos Biotechnology, Inc.
498 GAGCATCACTCTGACCATGATCATCACTCCCACCATAATCATGCTGCTTCTGGTAAAAAT	Db	; APPLICANT: Mack, David H. ; APPLICANT: Murray, Richard
119 119	Qy	
101 AspHisGLuHisHisSerAspHisGLuArgHisSerAspHisGLuHisHisHisHisSerAspHisGLuArgHisSerAspHisGLuHisHisHisHisHisHisHisHisHisHisHisHisHisH	dg VQ	Aziz, Na Ginsberg Gish, Ku
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81 AsnīleGlyīleAspLysIleLysArgIleHisIleHisHisAspHisAspHisHisSer	. Q	-10-29 Sequen
318 TTCTACCGCTATGGAGAAAATAATTCTTTGTCAGTTGAAGGGTTCAGAAAATTACTTCAA	дb	12
61 pheTyrArgTyrGlyGluAsnAsnSerLeuSerValGluGlyPheArgLysLeuLeuGln	δ	TITATTTCCAPATTTGAACATAAAATCGTGTTTTCGTATAAATTTC
258 GAATCTGGCATTAATGTTGACTTGGCAATTTCCACACGGCAATATCATCTACAACAGCTT	da b	288

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Query Match:
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APPLICANT: MUCK 20 STAID

APPLICANT: WALSON, SUSAN R.

APPLICANT: WALSON R.

APPLICANT: WALSON R.

APPLICANTON: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer FILE OF INVENTION REPORTS.

CURRENT APPLICATION NUMBER: US 09/663,733

PRIOR APPLICATION NUMBER: US 09/663,733

PRIOR FILLING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/330,366

PRIOR APPLICATION NUMBER: US 60/332,464

PRIOR APPLICATION NUMBER: US 60/334,393

PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR APPLICATION NUMBER: US 60/355,250

PRIOR APPLICATION NUMBER: US 60/356,714

PRIOR APPLICATION NUMBER: US 60/356,714

PRIOR APPLICATION NUMBER: US 60/356,714
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SEQ ID NO 838
LENGTH: 3461
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natas
APPLICANT: Ginsberg, W
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      AsnIleGlyIleAspLy8IleLy8ArgIleHi8IleHi8Hi8AspHi8AspHi8Hi8Ser
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Hevezi, Peter A.
Mack, David H.
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RESULT 14 US-10-295-027-878 Sequence 878, Application US/10295027 Publication No. US20030232350A1 GENERAL INFORMATION: APPLICANT: Afar, Daniel APPLICANT: Aziz, Natasha APPLICANT: Ginsberg, Wendy M. APPLICANT: Gish, Kurt C. APPLICANT: Glynne, Richard APPLICANT: Glynne, Richard APPLICANT: Hevezi, Peter A. APPLICANT: Mack, David H.	Qy 268 ArgTrpGlyTyrPhePheLeuGlnAsnAlaGlyMetLeuLeuGlyPheGlyIleMetLeu 287	2178 TANGCTGAAAATGTTTCTATGTGGATATTTGCACTTACTGCTGGCTTATTCATGTATGT	Qy 208 ASDALALEUSERALAMETLEUALATYLEUGLYMETALATHTGLYILEPHEILEGLYHis 227	Qy 188 LeuGlyAspPheAlaValLeuLeuLysAlaGlyMetThrValLysGlnAlaValLeuTyr 207	168	148 1938	Db 1818 TACCATCATATTCTCCATCATCACCACCACCACCACCATCCTCACAGTCACAGCCAG 1877 Qy 128 ArgTyrSerArgGluGluLeuLy8AspAlaGlyValAlaThrLeuAlaTrpMetValIle 147	1758 CATTCACATTTCCACGATACACTCGGCCAGTCAGACGATCTCATCACCACCATCATGAC 120	Db 1698 CATGCTCATCCACAGGAAGTCTACAATGAATATGTACCCAGAGGGTGCAAGAATAAATGC 1757 Qy 119	Db 1638 CCCTCCCACTTTGATTCTCAGCAGCCTGCAGTCTTGGAAGAAGAAGAGGTCATGATAGCT 1697 Qy 119 119	Db 1578 GAGGAGAAAGTAGATACAGATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAG 1637 Qy 119 119	Qy 119 119 Db 1518 GATGATGATGTGGAGATTAAGAAGCAGTTGTCCAAGTATGAATCTCAACCAAAT 1577 Qy 119 119

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1578 GAGGAGAAAGTAGATACAGATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAG 1637	119 119	1518 GATGATGATGTGGAGATTAAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAAT 1577	119 119	1458 CTCACATTGATCAAACAATTTAAAGATAAGAAGAAAAAGAATCAGAAGAAACCTGAAAAT 1517	119 119	1398 ACGTGGAAGGGTCTAACAGCTCTAGGAGGCCTGTATTTCATGTTTCTTGTTGAACATGTC 1457	119 119	1338 GGACCACTTTTCAGTCATCTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCC 1397	119 119	1278 TCTCATGCAAGTCACCACCATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGA 1337	119 119	1218 CTTGTGGCACTGGCCGTTGGGACTTTGAGTGGTGATGCTTTTTTTACACCTTCTTCCACAT 1277	119 119	1158 CTGGGGGTTATCTTAGTGCCTCTCATGAATCGGGTGTTTTTCAAATTTCTCCTGAGTTTC 1217	119 119	1098 TTACAAATAGCCTGGGTTGGTGGTTTTATAGCCATTTCCATCAGCTTTCCTGTCTCTG 1157	119 119	1038 AGATCTTGTCTGATTCATACAAGTGAAAAGAAGGCTGAAATCCCTCCAAAGACCTATTCA 1097	119 119	978 CCGCTGAATGCAACAGAGTTCAACTATCTCTGTCCAGCCATCATCAACCAAATTGATGCT 1037	119 119	918 CCTCAGGAGTGTTTCAATGCATCAAAGCTACTGACATCTCATGGCATGGGCATCCAGGTT 977	119 119	858 AATGAATCTGTGAGTGAGCCCCGAAAAGGCTTTATGTATTCCAGAAACACAAATGAAAAT 917	119 119	798 TCCACTCCACCCAGTGTCACATCAAAGAGCCGGGTGAGCCGGCTGGCT	119 119	738 TTTCTAGAGACAATAGAGACTCCAAGACCTGGAAAACTCTTCCCCAAAGATGTAAGCAGC 797	119 119	678 AGTGTTAGTGCTAGTGAAGTGACCTCAACTGTGTACAACACTGTCTCTGAAGGAACTCAC 737	119 119	618 AGCCAGGGGAAAGGAGCTCACCGACCAGAACATGCCAGTGGTAGAAGGAATGTCAAGGAC 677	119 119	558 AAGCGAAAAGCTCTTTGCCCAGACCATGACTCAGATAGTTCAGGTAAAGATCCTAGAAAC 617	119 119	498 GAGCATCACTCTGACCATGATCATCACTCTCACCATAATCATGCTGCTTCTGGTAAAAAT 557

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US-10-058-270A-29

(US-10-058-270A-29)

(Sequence 29, Application US/10058270A)

(Sequence 29, Application US20040029114A1)

(SENURRAL INFORMATION:

APPLICANT: Mack, David H.

APPLICANT: Afar, David H.

APPLICANT: Afar, Daniel

(APPLICANT: Afar, Daniel

(APPLICANT: Bos Biotechnology, Inc.

APPLICANT: Bos Biotechnology, Inc.

(TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer FILE REFERENCE: 018501-005210US

(CURRENT APPLICATION NUMBER: US/10/058,270A)

(CURRENT FILING DATE: 2001-01-24

PRIOR APPLICATION NUMBER: US 60/263,965

PRIOR APPLICATION NUMBER: US 60/265,928

PRIOR APPLICATION NUMBER: US 60/265,928

PRIOR APPLICATION NUMBER: US 60/265,928

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-04-09
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PRIOR FILING DATE: 2001-04-09
PRIOR PELICATION NUMBER: US 60/288,590
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,443
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 141
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-MODEL-frame+ p2n.model -DEV=xlh
-Q-/Ggn2_1/USPTO_epool/US10659004/runat_14032005_181236_15771/app_query.fasta_1.455
-DB=Issued_Patents_NA -QPMT=fastap_-SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STAAT=1 -END=-1 -NATRIX=blosum62 -TRANS=human40.cdi
-LIST45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10659004_@CGN 1 1 69 @runat 14032005 181236 15771 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG-SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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e 12147,	equence 15	e 12369,	equence 297, Ap	Sequence 6150, Ap	14613,	ω `	12214,	14327,	14326,	N	12384,	906, 7	8591,	16971,	12212,	6385,	17361	12147,	944, F	8863	e 4307,	14'928	236	e 198,	equence 1, Ag	equence 13765,	equence 12052,	e 1, Appl	e 55, App	equence 1979, A	Sequence 5631, Ap	equence 149, Ap

ALIGNMENTS

Alignment Scores:

Db 901 AGATCTTGTCTGATTCATACAAGTGAAAAGAAGGCTGAAATCCCTCCAAAGACCTATTCA 960	119	841 CCGCTGAATGCAACAGAGTTCAACTATCTCTGTCCAGCCATCATCAACCAAATTGATGCT 9	Qy 119 119	Db 781 CCTCAGGAGTGTTTCAATGCATCAAAGCTACTGACATCTCATGGCATGGGCATCCAGGTT 840	Qy 119 119	Db 721 AATGAATCTGTGAGTGAGCCCCGAAAAGGCTTTATGTATTCCAGAAACACAAATGAAAAT 780	Qy 119 119	661 TCCACTCCACCCAGTGTCACATCAAAGAGCCGGGTGAGCCGGCTGGCT	2y 119	119	Db 541 AGTGTTAGTGCTAGTGAAGTGACCTCAACTGTGTACAACACTGTCTCTGAAGGAACTCAC 600	Qy 119 119	Db 481 AGCCAGGGGAAAGGAGCTCACCGACCAGAACATGCCAGTGGTAGAAGGAATGTCAAGGAC 540	119	421 AAGCGAAAAGCTCTTTGCCCAGACCATGACTCAGATAGTTCAGGTAAAGATCCTAGAAAC	<u>, , , , , , , , , , , , , , , , , , , </u>	11	301 GMCCHARANGHTICHATICHANCHTIGHARGITCHATACHTIGHAGCHTCHATICHANGACHTCHATICHANGHTCHATICHATICHATICHATICHATICHATICHATICHA	101 AspHi	ATTAA	Qy 81 AsnīleGlyīleAspLysīleLysArgīleHislleHisHisAspHisAspHisHisSer 100	181,TTCTACCGCTATGGAGAAAATAATTCTTTGTCAGTTGAAGGG	61 PheTyrArgTyrGlyGluAsnAsnSerLeuSerValGluGlyPheArgLysLeuLeuGln	Db 121 GAARCTGGGATTAATGTTGACTTGGCAATTTCCAACAGGCAATATCATCTACAACAGCTT 180	61 CTICATGAACTAAAAGCAGCTGCTTTCCCCCAGACCACAGAAAAATTAGTCCGAAATTG	21 LeuHisGluLeuLysAlaAlaAlaPheProGlnThrThrGluLysIleSerProAsnTrp 4	1 ATGGCGAGGAAGTTATCTGTAATCTTGATCCTGACCTTTTGCCCTCTCTGTCACAAATCCC 6	1 MetAlaArgLysLeuSerVallleLeuIleLeuThrPheAlaLeuSerValThrAsnPro 2	US-10-659-004-104 (1-302) x US-09-642-034-4 (1-2268)	4 Gaps: 1	Reficelic Similarity: 30.80% Conservative: 1 Best Local Similarity: 39.87% Mismatches: 0 Onerv Match: 453	1356.50 Matches:): 4.79e-148 Length:
Qy 228 TyrAlaGluAsnValSerMetTrpIlePheAlaLeuThrAlaGlyLeuPheMetHisVal 247	Db 1981 AATGCATTGTCAGCCATGCTGGCGTATCTTGGAATGGCAACAGGAATTTTCATTGGTCAT 2040	Qy 208 AsnAlaLeuSerAlaMetLeuAlaTyrLeuGlyMetAlaThrGlyIlePheIleGlyHis 227	u	188 LeuGlyAspPheAlaValLeuLeuLysAlaGlyMetThrValLysGlnAlaValLeuTyr	GCTTATCAAGTGGTTTAAGTACTTCTGTTGCTGTGTCTGTC	168 GlvLenSerserGlvLenSerThrSerValAlaValPheCvaHisGluLeuProHisGlu	Oy 148 MeTGLYASDGLYLEURISASHTERGETABDGLYLEURIGITGCTGCTTTTACCGAR 1860	1741	128 ArgTyrSerArgGluGluLeuLysAspAlaGlyValAlaThrLeuAlaTrpMetVallIle	Db 1681 TACCATCATATTCTCCATCATCACCACCACCAAAACCATCCTCACAGTCACAGCCAG 1740	120BisHisProHisSerHisSerGln	ORDITACORODACIONACIONACIONACIONACIONACIONACIONACION	110		1501 CCCTCCCACTTTGATTCTCAGCAGCCTGCAGTCTTGGAAGAAGAAGACGTCATGATAGCT		Db 1441 GAGGAGAAAGTAGATACAGATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAG 1500	Qy 119 119	L	119 119	CTCACATTGATCAAACAATTTAAAGATAAGAAGAAAAAGAATCAGAAGAAACCTGAAAAT	Db 1261 ACGIGGAAGGGICIAACAGCICIAGGAGGCCIGIAIIICAIGIIICIIGIIAGAAAACAIGIC 1220	119 119	Db 1201 GGACCACTTTTCAGTCATCTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCC 1260	Qy 119 119	Db 1141 TCTCATGCAAGTCACCACCATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGA 1200	Qy 119 119	L	119	L	119		Qy 119 119

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Db	ρ	ממ	γQ	Db	Qy	DЬ	δ	дb	Q	dd	δ	DЬ	Ş	Db	Ş	ф	Ş	DЬ	δ	DЬ	δ	дь	γ0	Db	γo	ФФ	Q	Db	δ	Db 49	\$ 1	D 49	? 8		•
1338 GGACCACTTTTCAGTCATCTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCC 1397	119 119	1278 TCTCATGCAAGTCACCACCATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGA 1337	119 119	1218 CTTGTGGCACTGGCCGTTGGGACTTTGAGTGGTGATGCTTTTTTTACACCTTCTTCCACAT 1277	119 119	1158 CTGGGGGTTATCTTAGTGCCTCTCATGAATCGGGTGTTTTTCAAATTTCTCCTGAGTTTC 1217	119 119	1098 TTACAAATAGCCTGGGTTGGTGGTTTTATAGCCATTTCCATCAGCTTTCCTGTCTCTG 1157	119 119	1038 AGATCTTGTCTGATTCATACAAGTGAAAAGAAGGCTGAAATCCCTCCAAAGACCTATTCA 1097	119 119	978 CCGCTGAATGCAACAGAGTTCAACTATCTCTGTCCAGCCATCATCAACCAAATTGATGCT 1037	119 119	918 CCTCAGGAGTGTTTCAATGCATCAAAGCTACTGACATCTCATGGCATGGGCATCCAGGTT 977	119 119	858 AATGAATCTGTGAGTGAGCCCCGAAAAGGCTTTATGTATTCCAGAAACACAAATGAAAAT 917	119 119	798 TCCACTCCACCCAGTGTCACATCAAAGAGCCGGGTGAGCCGGCTGGCT	119 119	738 TTTCTAGAGACAATAGAGACTCCAAGACCTGGAAAAACTCTTCCCCAAAGATGTAAGCAGC 797	119 119	678 AGTGTTAGTGCTAGTGAAGTGACCTCAACTGTGTACAACACTGTCTCTGAAGGAACTCAC 737	119 119	618 AGCCAGGGAAAAGGAGCTCACCGACCAGAACATGCCAGTGGTAGAAGGAATGTCAAGGAC 677	119 119	558 AAGCGAAAAGCTCTTTGCCCCAGACCATGACTCAGATAGTTCAGGTAAAGATCCTAGAAAC 617	119 119	498 GAGCATCACTCTGACCATGATCATCACTCTCACCATAATCATGCTGCTTCTGGTAAAAAT 557	119 119	ASPALSOLIMA BRITANDE ASPARANTE MANAGEMENT ASPARANTE ASPA	AsoHisGluHisHisSerAsoHisGluAroHisSerAsoHisGluHisHisSerAso	81 ASDILEGIYLIEASDLYSLIELYSAXGILEHISHLSASDHISASDHISHISSET 100	ILLIAC COCIAL ISONOMANALANI ICII ISICASI ISIANSSSI ICASSANALI INCIICAN	the state of the s	

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US-08-311-023-1; Sequence 1, Application; Patent No. 5693465

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RESULT

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ACGTGGAAGGGTCTAACAGCTCTAGGAGGCCTGTATTTCATGTTTCTTGTTGAACATGTC 1457
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COUNTRY: USA
ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,023
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: Reg. No. 5693465 32,925
REFERENCE/DOCKET NUMBER: WCM.56
TELECOMPUNICATION INFORMATION:
TELEPHONE: 703/521-2297
TELEPAX: 703/685-0573
248425
ID NO: 1:
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APPLICANT: MANNING, David Lockwood
APPLICANT: NICHOLSON, Robert Ian
APPLICANT: GEB, Julia Margaret
APPLICANT: GEB, Christopher Douglas
FITLE OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF
FITLE OF INVENTION: BREAST TUMOURS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Young & Thompson
STREET: 745 South 23rd Street
CITY: Arlington
STATE: VA
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Best Local Similarity:
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TELEX: 248425
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1310 base pairs
TYPE: nucleic acid
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                                             AlaPheThrGluGlyLeuSerSerGlyLeuSerThrSerValAlaValPheCysHisGlu
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 4
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Percent Similarity:
Best Local Similarity:
                                                                                        ; LENGTH: 2404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-311-023-3
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                                                            Alignment Scores:
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Patent No. 5693465
GENERAL INFORMATION:
                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMMBER: US/08/311,023
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: Reg. No. 5693465 32,925
REGISTRATION CHART NUMBER: WCM.56
TELECOMMUNICATION INFORMATION:
TELEPAN: 703/685-0573
TELEPAN: 703/685-0573
                                                                                                                                                                                 TELEX: 248425
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NICHOLSON, ROBERT IAN
APPLICANT: GEE, Julia Margaret
APPLICANT: GREEN, Christopher Douglas
TITLE OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF
TITLE OF INVENTION: BREAST TUMOURS
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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RESULT 5
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    Alignment Scores: Pred. No.:
                                                              ; ORGANISM: Homo US-09-814-915A-29
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                                                                                                                                        SOFTWARE: Pa
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                                                                                                                                                                                                                                                                                         APPLICANT: Horwitz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
TITLE OF INVENTION: Thereto
                                                                                                                                                                                                                                     FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/214,870 PRIOR FILING DATE: 2000-06-28 NUMBER OF SEQ ID NOS: 108
                                                                                                   LENGTH: 45
TYPE: DNA
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                                                                                                                                                                                                                                                                                           Liu, Chenghua
Asundi, Vinod
Ren, Feiyan
Zhang, Jie
Zhao, Qing A.
                                                                 Zhou, Ping
Goodrich, Ryle
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Best Local Similarity:
Query Match:
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (374)..(841)
US-09-774-528-283
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      RESULT 7
US-09-3903-38
; Sequence 38, Application
; Patent No. 654863
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_I_genes Version 2.0
SEQ ID NO 283
LENGTH: 2229
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APPLICANT: Xue, Aidong J.
APPLICANT: Wehrman, Tom
APPLICANT: Weng, Jian-Rui
APPLICANT: Wang, Junrui
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drwanac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic
TITLE OF INVENTION: Polypeptides
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NAME/KEY: 8ig_peptide

LOCATION: 139..198

OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 5.00

OTHER INFORMATION: seq HLLAGFCVWVVLG/WV

NAME/KEY: polyA. signal

LOCATION: 1854..1859

NAME/KEY: polyA. site

LOCATION: 1873..1888
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PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
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TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET.050CP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/113,686 PRIOR FILING DATE: 1998-12-22
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HisValAlaLeuValAspMetValProGluMetLeuHisAsnAsp---
                                               AGCCTGGGCCCTGTCCCCTCACTCCCTGGGTGTTTTGGGGTCACTGCTGGGGTCTTCCTC
                                                                                                                                                                                    HisGluLeuGlyAspPheAlaValLeuLeuLysAlaGlyMetThrValLysGlnAlaVal 205
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                                                                                                                                                                                                                                                                                                         VallleMetGlyAspGlyLeuHisAsnPheSerAspGlyLeuAlaIleGlyAlaAlaPhe 165
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                                                             GlyHisTyrAlaGluAsnValSerMetTrpIlePheAlaLeuThrAlaGlyLeuPheMet 245
                                                                                                                                     LeuTyrAsnAlaLeuSerAlaMetLeuAlaTyrLeuGlyMetAlaThrGlyIlePheIle
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US-10-659-004-104 (1-302) x US-09-621-976-1342 (1-464)
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SOFTWARE: Patent.pm
SEQ ID NO 1342
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Patent No. 6639063
GENERAL INFORMATION:
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APPLICANT: Jobert, S.
APPLICANT: Giordano, J
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LOCATION: 325
OTHER INFORMATION: n=a
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LOCATION: 92..160
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 12
OTHER INFORMATION: seq RLLLLSLVSGALG/LG
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LOCATION: 92..412
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ORGANISM: Homo
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---AlaSerAspHisGlyCysSerArgTrpGlyTyrPhePheLeuGlnAsnAlaGlyMet 279
                                                                GICTICCICTATGIGGCCCTI
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GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 17382
LENGTH: 633
TYPE: DNA
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GRGANISM: Drosophila melanogaster
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APPLICANT: HOmburger et al.
APPLICANT: HOmburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2100
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
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SEQ ID NO 1621
LENGTH: 754
TYPE: DNA
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Patent No. 6703491
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GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16903

LENGTH: 754

TYPE: DNA

ORGANISM: Drosophila melanogaster

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                                                                             US-10-659-004-104 (1-302) x US-09-663-600A-149 (1-522)
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PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR APPLICATION NUMBER: 60/074,121
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PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR APPLICATION NUMBER: 60/096,116
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5631
LENGTH: 894
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LENGTH: 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: DIAGNOSTICS AND THERAF FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT FILING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR PILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Proteus
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                                                                                                                                                                                                                                                                                                                                                                                                              LeuAlaTrpMetValIleMetGlyAspGlyLeuHisAsnPhe---SerAspGlyLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HisSerHisSerGlnArgTyr---SerArgGluGluLeuLysAspAlaGlyValAlaThr 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HisSerAspHisGluArgHisSerAspHisGluHisHisSerAspHisHis-----Pro
     aThrGlyIlePheIleGlyHisTyrAlaGluAsnValSerMetTrpIlePheAlaLeuTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATTCACACGATCACCATCACTCTCACGACCATGATCATCACGACCATGGCCATCAC
                                                                             GATCATCATGCACATTCTCATGÁACATACTCATAGCCATGAACATGAACATAGCCATGAT
                                                                                                                                                                              GATGCACAGCAAAATGAAGCCCCAAGTGTTCCATGAGCATCATCATG-----
                                                                                                                                                                                                                             eCysHisGluLeuProHisGluLeuGlyAspPheAlaValLeuLeuLysAlaGlyMetTh
                                                                                                                                                                                                                                                                              ATCATTATTCATCATCACCATTACCATAATAGTGGCGATGTTCATCTCCATTTTTATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCACGGTCATCACCATCATCATGGGCATGATCATCATCATGAACACAATGCTACTCCA
                                                                                                                           rValLysGlnAlaValLeuTyrAsnAlaLeuSerAlaMetLeuAlaTyrLeuGlyMetAl
                                                                                                                                                                                                                                                                                                                            IleGlyAlaAlaPheThrGluGlyLeuSerSerGly-LeuSerThrSerValAlaValPh
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Matches:
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JOD time : 225 Becs	Search completed: March 20, 2005, 01:39:54	559 ATGTTAAAAATTGAGATGTACTGG 586	260 pAlaSerAspHisGlyCysSerArgTrpGlyTyrPhe 272	499 AACATGCATTATGGGCAAGGGGAAGCTGGTACTCATGCTCCCGGAATTAGCCAAAAACGA 558	240 rAlaGlyLeuPheMetHisValAlaLeuValAspMetValProGluMetLeuHisAsnAs 260	445 CACGAACATAGCCATGAACACGAAGAACAATTTAGTCCAGTTATTGATAATGAC 498

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-MODEL-frame+ p2n.model -DEV=x1h
-MODEL-frame+ p2n.model -DEV=x1h
-Q-/Ggn2 _1/USPTO_ spool/US10659004/runat_14032005_181235_15741/app_query.fasta_1.455
-DB=GenEmb1 -QFMT-fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0
-UNITS=blite -START=1 -END=-1 -MATRIX=blosun62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10659004_@CGN 1 1 3731 @runat_14032005 181235_15741 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    1359.5
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Ygapop 10.0 , Ygapext
Egapop 6.0 , Fgapext
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Copyright (c) 1993 - 2005 Compugen Ltd.
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0	4996	27410 Primer i	782979 Sequence	26739	5078	82030	9 Seque	01905 Homo	0 Ното вар	1158 Ното вар	anic	83 Mus	Mus	Mus	2880	eque	091	4949 Segue	3909	7275	91400 Seque	9498 Ното вар	6260	6	ŝ	Seguer	32 Human n	N	1 Sequence 1	780	Sequence	08317 Homo	71697 Mus musc	05501;	720	_	~	_	٠.	w

ALIGNMENTS

	CDS	source	FEATURES	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	CQ834422
/note="unnamed protein product" /codon_start=1 /protein_id="CAH05426.1" /protein_id="CAH05426.1" /db_xref="GI:50833960" /translation="MARKLSVILILTFALSVTNPLHELKAAAFPQTTEKISPNWESGI /translation="MARKLSVILILTFALSVTNPLHELKAAAFPQTTEKISPNWESGI NVDLAISTRQYHLQQLFYRYGENNSLSVEGFRKLLQNIGIDKIKRIHIHHDHDHHSDH	/mol_type="unassigned DNA" /db_xref="taxon:9606" 138.	12744	Asahi Kasei Pharma Corporation (JP) Location/Qualifiers	Patent: WO 2004058805-A 293 15-JUL-2004;	T cell activating gene	Matsuda, A. and Yoneta, S.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	Homo sapiens (human)	•	CQ834422.1 GI:50833959	CQ834422	Sequence 293 from Patent WO2004058805.	CQ834422 2744 bp DNA linear PAT 29-JUL-2004	

EHHSDHERHSDHEHHSDHNHAASGKNKRKALCPDHDSDSSGKDPRNSQGKGA
HRPEHASGRRNVKDSVSASEVTSTVYNTVSEGTHFLETIETPRPGKLFPKDVSSSTPP
SVTSKSRVSRLAGRKTNESVSEPRKGFRYSRNTNENPODEFRASKLLTSHGMGIQVPL
NATEFNYLCPAIINQIDARSCLIHTSEKKAEIPPKTYSLJIAWVGGFIAISIISFLSL
LGVILVPLMNRVFFKFLLSFLVALAVGTLSGDAFLHLLPHSHASHHHSHSHEEPAMEM
KRGPLFSHLSSQNIEESAYFDSTWKGLTALGGLYFMFLVEHVLTLIKQFKDKKKKNQK

	. Qy 119 119
	Db 798 ACATCAAAGAGCCGGGTGAGCCGGCTGGCTGGTAGGAAAACAAATGAATCTGTGAGTGA
1878 CTGAAAGATGCCGGCGTCGCCACTTTGGCCTGGATGGTGATAATGGGTGATGACCCTGCAC	Qy 119 119 Db
134 LeuLysAspAlaGlyValAlaThrLeuAlaTrpMetVallleMetGlyAspGlyI	Db 738 ACTCCAAGACCTGGAAAACTCTTCCCCCAAAGATGTAAGCAGCTCCACCCAGTGTC 797 Qy
	Qy 119 119 pb
120HisHisProHisSerHisSerGinArgTyrSerArgG	Db 678 GTGACCTCAACTGTGTACAACACTGTCTCTGAAGGAACTCACTTTCTAGAGACAATAGAG 737 Qy
1758 ACACTCGGCCAGTCAGACGATCTCATTCACCACCATCATGACTACCATCATATTCTCCAT	Qy 119 119 Db
119	Db 618 CACCGACCAGAACATGCCAGTGGTAGAAGGAATGTCAAGGACAGTGTTAGTGCTAGTGAA 677 Qy
1698 GTCTACAATGAATATGTACCCAGAGGGTGCAAGAATAAATGCCATTCACATTTCCACGAT	Qy 119 119 Db
119	Db 558 CCAGACCATGACTCAGATAGTTCAGGTAAAGATCCTAGAAACAGCCAGGGGAAAGGAGCT 617 Qy
1638 CAGCAGCCTGCAGTCTTGGAAGAAGAAGAGGTCATGATAGCTCATGCTCATCCACAGGAA	
119	GAGCATCACTCTGACCATAATCATGCTGCTTCTGGTAAAAATAAGCGAAAAGCTCTTTGC 55
1578 GATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAGCCCTCCCACTTTGATTCT	119
119	438 GACCACGAGCAICACICAGACCAIGAGCGICACICAGACCAIGAGCAICACICAGACCAC
1518 AAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAATGAGGAGAAAGTAGATACA	10
119	378 ARTATAGGCATAGATAAAGAATCCATATACACCATCACCACCACCACCACCACCACCAC
1458 TTTAAAGATAAGAAAAAAAAGAATCAGAAGAAACCTGAAAATGATGATGATGTGGAGATT	### ##################################
119	0. 1
1398 GCTCTAGGAGGCCTGTATTTCATGTTTCTTGTTGAACATGTCCTCACATTGATCAAACAA 1457	### ##################################
119	23 GAAICIGGCAIIAAIGIIGACAATTACOOCTAATATTACAATTAC
1338 CTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCCACGTGGAAGGGTCTAACA 1397	4. π
119	198 CTTCATGAACGAAGCTGCTTTCCCCCAGACCACTGAGAAAATTTAGTCCGAATTGG 20
1278 CATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGAGGACCACTTTTCAGTCAT	25) LINE 470 COLD SELECT COLD COLD COLD COLD COLD COLD COLD COLD
119	138 AIGGCGAGGAAGIIAICIGIAANICIIGAACCIGACCIIIGCCCICICIGACCIGAC
1218 GGGACTTTGAGTGGTGATGCTTTTTTACACCTTCTTCCACATTCTCATGCAAGTCACCAC	0.0.0.4.4.4.4.4.0.0.0.0.0.0.0.0.0.0.0.0
119	-10-659-004-
1158 CCTCTCATGAATCGGGTGTTTTTCAAATTTCTCCTGAGTTTTCCTTGTGGCACTGGCCGTT	o Gapa:
119	ry Match: \$5.02%
1098 GGTGGTTTTATAGCCATTTCCATCATCAGTTTCCTGTCTCTGCTGGGGGGTTATCTTAGTG	ent Similarity: 40.32% Conserve:
119	ent Scores: 5.5e-112 Length:
1038 ACAAGTGAAAAGAAGGCTGAAATCCCTCCAAAGACCTATTCATTACAAATAGCCTGGGTT 1097	•
119	HKIVERINE" AUVUMVERMINIMADING ORMGIF E UQMAGRILLUGE GARILLIGATE UQMAGRILLUGE GARILLIGAT U
978 TTCAACTATCTCTGTCCAGCCATCATCAACCAAATTGATGCTAGATCTTGTCTGATTCAT	AVECHBLEHBLGDFAVLYARIVARMVINGUGLHRIK SUGHALGAFA E LGGUSSGUG SOV AVECHBLEHBLGDFAVLYARIVAR ONLY LYMATGIF E IGHUSSGUG SOVI AVECHBLEHBLGDFAVLYARIVAR ONLY LONG TO THE TOTAL OF THE
119	KPENDDVKIKKOLSKI KOLDTINKEK VUTUKI EGI LIKHUSQE SITI USQUFA VILBE EEVMI AHAH POEVYNEYV PROCKNIKCH SHOHT USQUBDI I HHHHD VHHI I LHHHHON QY
A18 GCWICKWARGCIWCIGWCWICICWIGGCWIGGGGGGGGGGGGGGGGGG	KRGPLFSHLSSQNIEESAYFDSTWKGLTALGGLYFWFLVEHVLTLIKOFKDKKKKNQK

1878 CTGAAAGATGCCGGCGTCGCCACTTTGGCCTGGATGGTGATAATGGGTGATGGCCTGCAC 1937	В	
GlyValAlaThrLeuA	δ	
1818 CATCACCACCAAAACCACCATCCTCACAGTCACAGCCCAGCCCTACTCTCGGGAGGAG 1877	В	
120HisHisProHisSerHisSerGlnArgTyrSerArgGluGlu 133	Q	
1758 ACACTOGGCCAGTCAGACGATCTCATTCACCACCATCATGACTACCATCATATTCTCCAT 1817	ర్జ	
119 119	Qγ	
1698 GTCTACAATGAATATGTACCCAGAGGGTGCAAGAATAAATGCCATTCACATTTCCACGAT 1757	Дb	
119 119	Ş	
1638 CAGCAGCCTGCAGTCTTGGAAGAAGAAGAGGTCATGATAGCTCATGCTCATCCACAGGAA 1697	Дb	
119 119	δ	
1578 GATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAGCCCTCCCACTTTGATTCT 1637	DЬ	
119 119	Qγ	
1518 AAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAATGAGGAGAAAGTAGATACA 1577	дb	
119 119	Qy	
1458 TTTAAAGATAAGAAGAAAAGAATCAGAAGAAACCTGAAAATGATGATGATGTGGAGATT 1517	Db	
119 119	γQ	
1398 GCTCTAGGAGGCCTGTATTTCATGTTTCTTGTTGAACATGTCCTCACATTGATCAAACAA 1457	Db	
119 119	Qy	
1338 CTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCCACGTGGAAGGGTCTAACA 1397	Db	
119 119	8	
1278 CATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGAGGACCACTTTTCAGTCAT 1337	몂	
119 119	δ	
1218 GGGACTTTGAGTGGTGATGCTTTTTTACACCTTCTTCCACATTCTCATGCAAGTCACCAC 1277	Db dd	
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1158 CCTCTCATGAATCGGGTGTTTTTCAAATTTCTCCTGAGTTTCCTTGTGGCACTGGCCGTT 1217	dg .:	
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1098 GGTGGTTTTATAGCCATTTCCATCATCAGTTTCCTGTCTCTGCTGGGGGGTTATCTTAGTG 1157	д ь :	
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1038 ACAAGTGAAAAGAAGGCTGAAATCCCTCCAAAGACCTATTCATTACAAATAGCCTGGGTT 1097	р ь	
119 119	Qy	
978 TTCAACTATCTCTGTCCAGCCATCATCAACCAAATTGATGCTAGATCTTGTCTGATTCAT 1037	Db	
119 119	Qy	
918 GCATCAAAGCTACTGACATCTCATGGCATGGGCATCCAGGTTCCGCTGAATGCAACAGAG 977	Db	
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858 CCCCGAAAAGGCTTTATGTATTCCAGAAACACAAATGAAAATCCTCAGGAGTGTTTCAAT 917	망	

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Green, C., Gilhooly, E.M.
Direct Submission
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Box 147, Liverpool L69 3BX, UK
On Feb 8, 2001 this sequence ve
Location/Qualifiers
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HRPEHASGRRINVSJVSASEVYSTVNITVSEOTHFLETIETFRFGKLFPKDVSSSTPP
SVTSKSRVSBLAGRKTINESVSESPRKGFMYSRNTINENPOECFNASKLLTSHGMGIOVFL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1	Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;	VERSION AX511618.1 GI:23392426 KEYWORDS	Sequence 25 from Patent WO02055705. AX511618	3445	***************************************	CA 298	222	268 ArgTrpGlyTyrPhePheLeuGlnAsnAlaGlyMetLeuLeuGlyPheGlyIleMetLeu	Db 2238 GCTCTGGTTGATATGGTACCTGAAATGCTGCACAATGATGCTAGTGACCATGGATGTAGC 2297	Qy 248 AlaLeuValAspMetValProGluMetLeuHisAsnAspAlaSerAspHisGlyCysSer 267	Db 2178 TATGCTGAAAATGTTTCTATGTGGATATTTGCACTTACTGCTGGCTTATTCATGTATGT	Qy 228 TyralaGluAsnValSerMetTrpIlePheAlaLeuThralaGlyLeuPheMetHisVal 247	Db 2118 AATGCATTGTCAGCCATGCTGGCGTATCTTGGAATGGCAACAGGAATTTTCATTGGTCAT 2177	Qy 208 AsnAlaLeuSerAlaMetLeuAlaTyrLeuGlyMetAlaThrGlyIlePheIleGlyHis 227	Db 2058 TTAGGTGACTTTGCTGTTCTACTAAAGGCTGGCATGACCGTTAAGCAGGCTGTCCTTTAT 2117	188 LeuGlyAspPheAlaValLeuLeuLysAlaGlyMetThrValLysGlnAlaValLeuTyr	GGCTTATCAAGTGGTTTAAGTACTTCTGTTGCTGTGTTCTGTCATGAGTTGCCTCATGAA	168 GlyLeuSerSerGlyLeuSerThrSerValALaValPheCy8H18Gl1LeuPrCH18GlU	1938 ATGGGTGATGGCCTGCACAATTTCAGCGATGGCCTAGCAATTGGTGCTGCTTTTACTGAA	148 MetGlyAspGlyLeuHisAsnPheSerAspGlyLeuAlaIleGlyAlaAlaPheThrGlu	1878 CGCTACTCTCGGGAGGAGCTGAAAGATGCCGGCGTCGCCACTTTGGCCTGGATGGTGATA	128 ArgTyrSerArgGluGluLeuLysAspAlaGlyValAlaThrLeuAlaTrpMetValIle	1818 TACCATCATATTCTCCATCATCACCACCAAAACCACCATCCTCACAGTCACAGCCAG	120	Db 1758 CATTCACATTTCCACGATACACTCGGCCAGTCAGACGATCTCATTCACCACCATCATGAC 1817	Qy 119 119	Db 1698 CATGCTCATCCACAGGAAGTCTACAATGAATATGTACCCCAGAGGGTGCAAGAATAAATGC 1757	Qy 119 119	Db 1638 CCCTCCCACTTTGATTCTCAGCAGCCTGCAGTCTTGGAAGAAGAAGAAGATCATGATAGCT 1697	Oy 119 119	Db 1578 GAGGAGAAAGTAGATACAGATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAG 1637	Оу 119 119	Db 1518 GATGATGATGTGGAGATTAAGAAGCAGTTGTCCAAGTATGAATCTCAACTATCAACAAAT 1577	Qy 119 119

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		LeuHisGluLeuLvsAlsAlsAlsPheProGlnThrThrGluLvsIleSerProAsnTrn	73 ATGGCGAAGTTATCTGTAATCTTGATCCTTGACCTTTTGCCCTCTCTTCACAAATCCC 132	1 Met AlaArqiyai,euserVallleieusleichthrabaalaieuserValThrasnoro	-659-004-104 (1-302) x AX207207 (1-2776)	Query Match: 84.40% Indels: 453 DB: 6 Gaps: 1	Allarity: 39.87% Conservative: Similarity: 39.74% Mismatches:	4.41e-111 1349.50	ment Scores:	ORIGIN /db_xref="taxon:9606"		EATURES Location/Qualifiers source 1. 2776	AL Patent: WO 0155178-A 3 02-AUG-2001; GENERYTECH INC (US)	AUTHORS Goddard, A., Gurney, A.L., Smith, V., Hongo, J.A. and de Sauvage, F. TITLE Compositions and methods for treatment of cancer		NISM Homo sapiens Eukaryota; Metazoa; Chordata;	Ното варіеля	1 GI:15394961	AX207207 2776 bp DNA linear PAT 30-AUG-2001 ITION Sequence 3 from Patent WO0155178.	RESULT 8 AX207207	2337 CTTATTTCCATATTTGAACATAAAATCGTGTTTCGTATAAATTTC 2381	288 LeuIleSerIlePheGluHisLysIleValPheArgIleAsnPhe 302 	2277 CGCTGGGGTATTTCTTTTTACAGAATGCTGGGATGCTTTTGGGTTTTGGAATTATGTTA 2336	268 ArgTrpGlyTyrPhePheLeuGlnAsnAlaGlyMetLeuLeuGlyPheGlyIleMetLeu 287	2217 GCTCTGGTTGATATGGTACCTGAAATGCTGCACAATGATGCTAGTGACCATGGATGTAGC 2276	248 AlaLeuValAspMetValProGluMetLeuHisAsnAspAlaSerAspHisGlyCysSer 267	228 TyrAlaGluAsnValSerMetTrpIlePheAlaLeuThrAlaGlyLeuPheMetHisVal 247	AATGCATTGTCAGCCATGCTGGCTATCTTGGAATGGCAACAGGAATTTTCATTGGTCAT	208 AsnAlaLeuSerAlaMetLeuAlaTyrLeuGlyMetAlaThrGlyIlePheIleGlyHis 227	188 LeuGlyAspPheAlaValLeuLeuLysAlaGlyMetThrValLysGlnAlaValLeuTyr 207 	1977 GGCTTATCAAGTGGTTTAAGTACTTCTGTTGCTGTGTTCTTGTCATGAGTTGCCTCATGAA 2036	CLYLEUSETSETU VLEUSET TYSETVA A AVAILURE VEH SCIII DIUTOH SCIII
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etValile etValile etValile rodication rodication rodication roman 18 rohisGlu 16 rodication rodicat	1 MetAlaArgLysLeuSerVallleLeuIleLeuThrPheAlaLeuSerValThrAsnPro 20	59-004-104 (1-302) x AX207205 (1-3461	t Scores: 1.51e-107 Length: 346 1311.50 Matches: 299 Similarity: 40.05% Conservative: 1 al Similarity: 39.92% Mismatches: 2 tch: 82.02% Indels: 449 6 Gaps: 1	CE Addard, A Gurney, A.L., Smith, V., Hongo, J.A. and de Sauvage, Compositions and methods-for treatment of cancer AL Patent: WO 0155178-A 1 02-AUG-2001; GENENTECH, INC. (US) Location/Qualifiers 1 .3461 /organism="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606"	AX207205 Sequence 1 from Patent WO0155178.) AX207205 AX207205 AX207205.1 GI:15394960 Homo sapiens (human) Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	288 LeuileSerilePheGluHisLygileValPheArgileAgnPhe 302	268 ArgTrpGlyTyrPhePheLeuGlnAsnAlaGlyMetLeuLeuGlyPheGlyIleMetLeu 287 	248 AlaLeuValAspMetValProGluMetLeuHisAsnAspAlaSerAspHisGlyCysSer 267	228 TyralaGluAsnValSerMetTrpIlePheAlaLeuThralaGlyLeuPheMetHisVal 247	208 AsnalaLeuSerAlaMetLeuAlaTyrLeuGlyMetAlaThrGlyIlePheIleGlyHis 227	188 LeuGlyAspPheAlaValLeuLeuLysAlaGlyMetThrValLysGlnAlaValLeuTyr 207 	168 GlyLeuSerSerGlyLeuSerThrSerValAlaValPheCy8Hi8GluLeuProHi8Glu 18 	148 MetGlyAspGlyLeuHisAsnPheSerAspGlyLeuAlaIleGlyAlaAlaPheThrGlu 167	128 ArgTyrSerArgGluGluLeuLysAspAlaGlyValAlaThrLeuAlaTrpMetValIle 147

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294 HisLysIleValPheArgIleAsnPhe 302	2298 TTACAGAATGCTGGGATGCTTTTGGGTTTTGGAATTATGTTACTTAT-TCCATATTTGAA 2356	LeuGlnAsnAl		ProGluMetLeuHisAsnAspAlaSerAspHisGlyCysSerArgTrpGlyTyrPhePhe 2	ATGTGGATATTTGCACTTACTGCTGGCTTATTCATGTATGT	MetTrpIlePheAlaLeuThrAlaGlyLeuPheMetHisValAlaLeuValAspMetVal 2	CTGGCTATCTTGGAATGGCAACAGGAATTTTCATTGGTCATTATGCTGAAAATGTTTCT 21	المارة	TARCHARARGERATCARCETTARAGERAGERETETTTTTTTTTTTTTTTTTTTTTTTT	Telling and aglymorThrvallysglnalaValLeuTyrAsnalaLeuSerAlaMet	174 Serinzbervalatavalene Venteu Ludurburundung yaspermanava 122	MAILICANG COMING CCLANG CAMELANG AND	154 AmphaserAmpdiyLouAlalleGlyAlaAlaphamingiuGlyLouberSerotyLou 1/3	CAMPANATION		i.e	CATCACCACCAAAAACCACCATCCTCACAGTCACAGCCAGC	HigHigProHigSerHigSerGlnArgTyrSerArgGluGlu 1	ACACTCGGCCAGTCAGACGATCTCATTCACCACCATCATGACTACCATCATATTCTCCAT	119	1698 GTCTACAATGAATAIGTACCCAGAGGGTGCAAGAATAAATGCCATTCACATTTCCACGAT 1757	119	1638 CAGCAGCCTGCAGTCTTGGAAGAAGAAGAGGTCATGATAGCTCATGCTCATCCACAGGAA 1697	119	1578 GATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAGCCCTCCCCACTTTGATTCT 1637	119 119	1518 AAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAATGAGGAGAAAGTAGATACA 1577	119 119	1458 TTTAAAGATAAGAAGAAAAAGAATCAGAAGAAACCTGAAAATGATGATGATGTGGAGATT 1517	119 119	1398 GCTCTAGGAGGCCTGTATTTCATGTTTCTTGTTGAACATGTCCTCACATTGATCAAACAA 1457	119 119	1338 CTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCCACGTGGAAGGGTCTAACA 1397	119 119	1278 CATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGAGGACCACTTTTCAGTCAT 1337	119 119

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REFERENCE
AUTHORS
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TITLE
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Bource
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RS Strausbergy R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
RIAUSBERGY, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Gaithersburg, Maryland;
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                             Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 116 Row: g Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20982834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-JUL-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC055012

3610 bp mRNA linear ROD 21-OCT-200 Mus musculus solute carrier family 39 (metal ion transporter), member 6, mRNA (cDNA clone MGC:62673 IMAGE:6337369), complete cds.
                                                                                                                                                                                                                                                                           Young, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                  Zhang, L.-H. and Green, E.D.
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                                                                                                                                                                                                              LeuHisGluLeuLysAla---AlaAlaPheProGlnThrThrGluLysIleSerProAsn
                                                                                                                                                                                                                                                                                ATGGCCACAGATTTATCTGTAATCATGATCTTGACCTTTTGCCCTTTTGGGTTACAAGCCCCC
LeuPheTyrArgTyrGlyGluAsnAsnSerLeuSerValGluGlyPheArgLysLeuLeu 79
                                                                                                       TrpGluSerGlyIleAsnValAspLeuAlaIleSerThrArgGlnTyrHisLeuGlnGln
                                                                                                                                                                   TGGGAACCTGGTGTTAATGTTGACTTGGCAGTTACCATGCAGCGACACCATCTGCAGCAG
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SGKNPRTSLGKGSRPAEHMNGRRNIKESASSSESVTSAVNVVSBEGTRFVETIETPKPG
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ATGIFIGHYAENVSMMIFALTAGLFMYVALVDMVPEMLHNDASDHGCSRWGYFFLQNA
GILLGFGIMLLISIFEHKIVFRINF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Slc39a6"
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codon_start=1
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db_xref="LocusID:106957"
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1237.50
38.43%
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Matches:
Conservative:
Mismatches:
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Qy 298 PheArgIleAsnPhe 302	Qy 258 HisAsnAspAlaSerAspHisGlyCysSerArgTrpGlyTyrPhePheLeuGlnAsnAla 277		Qy 178 AlaValDheCysHisGluLeuProHisGluLeuGlyAspPheAlaValLeuLeuLysAla 197 [TCCGACGACCTCATCCACCACCATCACGACTACCATCACATTCTGCACCACCACCACCACCACCACCACCACCACCACCACCAC	119 1771 ATGTT 119 119	DB 14/1 AATATAGARAGARAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA

Qy во GlaasnileGlyIleAspLysIleLysArgIleHisIleHisHisAspHisAspHisHis 99	Qy 60 LeuPheTyrArgTyrGlyGluAsnAsnSerLeuSerValGluGlyPheArgLysLeuLeu 79	יט יטטטארייטטאטיותאוטיוטאראטיוטיוטטראטיוערעוטראטרעט י		40 TrnGluSerGlvIleAenValAenLeuBlaIleSerThr&rnGlnTvrHdeLeuGlnGlnGln		21 LeuHisGluLeuLysAlaAl	-10-659-004-104 (1-302) x AB071697 (1-3287)	y Match: 71.79% Indels: 10 Gaps:	t Similarity: 37.35% ocal Similarity: 35.18%	6.49e-93 Length: 1148.00 Matches:	Alignment Scores:	ALVDMVPEMLHNDASDHGCSRWGYFFLQNAGILLGFGIMLLISIFEHKIVFRINF"	EELKDAGIATLAMMVIMGDGLHNFSDGLAIGAAFTEGLSSGLSTSVAVFCHELDHELG DFAVLLKAGMTVVOAVLLYNALSAVLAYLGMATGIFIGHVAENVSWAIFALTAGIFRYVV	QLSKYDSQLSSNEEKVDPGERPESYLRADSQEPSPFDSQQPTMLEEEEEVMIAHAHPQE VYNEYVPRGCKNKCHSHFHDTLGOSDDLLHHHHYHHILLHHHHHHNHHPHSGSVSB	FFKFLLSFLVALAVGTLSGDALLHLLPHSHASHQHSHSHBBPAMEMKRGPLFSHLSAQ NIBBSSYFDSTWKGLTALGGLYFMFLVEHVLTLIKOFKDKKKKNOKKPENDEDVESKK	/translation="mysrnindniqecenttkiltshgmsiqallnateenylcpaii NQIDARACLIHTASEKKAEIPPKTYSLQIAWLGGFIAISIISFLSLLGVILVPLMNRV	/protein id="BAB86300.1" /protein id="BAB86300.1" /db xref="GI:19570346"	/product="endoplasmic reticulum membrane protein"	CDS 7042221 /gene="ermelin"		<pre>/cell_type="gkeletal muscle myoblasts" /clone lib="lambda ZAPII C2 myoblast cDNA"</pre>	/db xre="taxn:10090" /db xre="taxn:10090" /cell line="C2"		FEATURES Location/Qualifiers	Chiba 263-8522, Japan (E-mail:tendo@cuphd.nd.chiba-u.ac.jp, Tel:81-43-290-3911, Fax:81-43-290-3911)	ĄĽ	Endo, T.		JOURNAL Gene 284 (1-2), 31-40 (2002) MEDLINE 2188618	Ermelin, a	and Endo. T.	Euka	SOURCE Mus musculus (house mouse) ORGANISM Mus musculus	VERSION AB071697.1 GI:19570345 KEYMORDS	DEFINITION Mus musculus ermelin mRNA for endoplasmic reticulum membrane protein, complete cds.
Qy 119	1202	Оу 119	Db 1142 GAAATGAAAA	Оу 119	Db 1082 CTTCTCCCAC	Оу 119	Db 1022 CTGCTGAGCT	Ογ 119	Db 962 TTCCTGTCTC	Оу , 119	Db 902 AAGACCTATT	Оу 119	Db 842 ATTGATGCTC	Оу 119	Db 782 ATCCAGGCTC	Qу 119	Db 722 AATGACAATA	Оу 119	Db 662 AAGAAAAGCA	Оу 119	Db 602 TCTACCCCAC	Оу 119	Db 542 TCGCTTTGTA	Qy 119	Db 482 GGAGAGTGCA	Qу 119	Db 422 AACTAGTCTA	Оу 119	Db 362 AAACAATCGG	Оу 119	Db 302 CCACGAGCAT	Оу 119	Db 243 GCTGACCACC	Qy 100 SerAspHisc	Db . 183 CAGAACATAG
	TATTTTGATTCCACGTGGAAAGGTCTGACGGCTCTAGGGGGCTTATATTTCATGTTTCTT 1261	119	GAAATGAAAAGAGGCCCCCTGTTCAGCCACCTGTCGGCTCAGAATATAGAAGAAAGCTCC 1201	119	CTTCTCCCACACTCTCATGCAAGTCATCAGCACAGTCATAGCCATGAAGAGCCAGCGATG 1141		CTGCTGAGCTTCCTCGTGGCGCTGGCCGTCGGAACGCTGAGTGGCGATGCTCTGTTACAT 1081	119	TTCCTGTCTGTGGGAGTCATCTTGGTGCCACTCATGAACCGGGTATTTTTCAAGTTC 1021	119	AAGACCTATTCTTTACAAATAGCCTGGCTTGGTGGCTTCATAGCCATTTCCATCATCAGT 961		ATTGATGCTCGGGCTTGTCTGATTCATACAGCAAGTGAGAAGAAGGCAGAAATCCCTCCA 901	119	ATCCAGGCTCTGTTGAATGCAACGGAATTTAACTATCTCTGCCCAGCCATCATCAATCA		AATGACAATATTCAGGAGTGTTTCAATACAACCAAGCTGCTGACATCCCATGGCATGAGC 781	119	AAGAAAAGCAATGAGTCTGTGAGTGAGCCCAGAAAGAGCTTTATGTATTCCAGAAACACA 721	119	TCTACCCCACCCAGCATCACGGAGAAAAGCCGAGTGGGCCGGCTGAGTCGGCTAGCTA		TCGCTTTGTAGAGACAATAGAGACTCCAAAACCTGGGAGACGCACCAAAGATGTAAACCT 601	119	GGAGAGTGCAAGCTCTAGTGAAGTGACCTCGGCGGTATACAACGCTGTCTCTGAAGGAAC 541		AACTAGTCTAGGGAAAGGATCTCGCCCAGCAGAGCACATGAATGGTAGGAAGGA	119	AAACAATCGGAAAGCCTTTTGTCCAGACCTTGACTCTGATAATTCAGGTAAAAATCCTAG 421	119	CCACGAGCATCACTCGGACCACGAGCACCATTCCCACCGCAGTCACACGGTTGCTGGTAA 361		GCTGACCACGAGCATCACTCGGACCATGAGCATCACTCGGACCACGAGCATCACTCGGA- 301	SerAspHisGluHisHisSerAspHisGluArgHisSerAspHisGluHisHisSerAsp 119	

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2212 bp mRNA linear PRI 04-NOV-2003
Homo sapiens solute carrier family 39 (zinc transporter), member 6,
mRNA (cDNA clone IMAGE:3343159), partial cds.
                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                              BC008317.2 GI:34782897
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MEDLINE
PUBMED
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CE 1 (bases 1 to 2212)

1 (bases 1 to 2212)

Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J.G.,

RS Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J.G.,

RS Strausberg, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,

Dlatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,

Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,

Carrinci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,

McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S. W.,

Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,

Fahey, J., Helton, E., Ketteman, M., Gay, L. J., Hulyk, S. W.,

Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,

Fahey, J., Helton, E., Ketteman, M., Woung, A. C., Shevchenko, Y.,

Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,

Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E.,

Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDMA sequences
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
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Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
On Sep 16, 2003 this sequence version replaced
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Proc. Natl. Acad. Sci. U.S.A. S
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is from the Arabidopsis thaliana ZIP protein family these
proteins are responsible for zinc uptake in the plant.
Also found within this family are C. elegans proteins of
unknown function which are annotated as being similar to
human growth arrest inducible gene product, although this
protein in not found within this family"
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/note="Zip; Region: ZIP Zinc transporter. The ZIP family
/note="Zip; Region: ZIP Zinc transporter."
consists of zinc transport proteins and many putative
metal transporters. The main contribution to this family
is from the Arabidopsis thaliana ZIP protein family these
proteins are responsible for zinc uptake in the plant.
Also found within this family are C. elegans proteins of
unknown function which are annotated as being similar to
human growth arrest inducible gene product, although this
protein in not found within this family"
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Patent: WO 2004058805-A 431 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)
Location/Qualifiers
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T cell activating gene
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                                                                                                                                         LysIleLysArgIleHisIleHisHisAspHisAspHisHisSerAspHis-----Glu 103
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SerHisSerGlnArgTyrSerArgGluGluLeuLysAspAlaGlyValAlaThrLeuAla 143
                                             CATGGATGTAGCCGCTGGGGGTATTTCTTTTTACAGAATGCTGGGATGCTTTTTGGGTTTT
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Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,
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Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
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Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 2815)
1 (bases 1 to 2815)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC054780

Mus musculus endoplasmic reticulum Clone IMAGE:6813896), partial cds.
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BC054780.1
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Submitted (01-JUL-2003) National Institutes of Health, Mammalian
                         Strausberg, R.
Direct Submission
                                                                                                                                                              human and mouse cDNA sequences proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaValLeuTyrAsnAlaLeuSerAlaMetLeuAlaTyrLeuGlyMetAlaThrGlyIle 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuProHisGluLeuGlyAspPheAlaValLeuLeuLysAlaGlyMetThrValLysGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTTTTACTGAAGGCTTATCAAGTGGTTTAAGTACTTCTGTTGCTGTGTTCTGTCATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaPheThrGluGlyLeuSerSerGlyLeuSerThrSerValAlaValPheCysHisGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAATTATGTTACTTATTTCCATATTTGAACATAAATCGTGTTTCGTATAAATTTC 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyIleMetLeuLeuIleSerIlePheGluHisLysIleValPheArgIleAsnPhe 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATGGATGTAGCCGCTGGGGGTATTTCTTTTTACAGAATGCTGGGATGCTTTTGGGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisGlyCysSerArgTrpGlyTyrPhePheLeuGlnAsnAlaGlyMetLeuLeuGlyPhe 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCATGTATGTTGCTCTGGTTGATATGGTACCTGAAATGCTGCACAATGATGCTAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheMetHisValAlaLeuValAspMetValProGluMetLeuHisAsnAspAlaSerAsp 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCATTGGTCATTATGCTGAAAATGTTTCTATGTGGATATTTGCACTTACTGCTGGCTTA 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheIleGlyHisTyrAlaGluAsnValSerMetTrpIlePheAlaLeuThrAlaGlyLeu 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGTCCTTTATAATGCATTGTCAGCCATGCTGGCGTATCTTGGAATGGCAACAGGAATT
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                                                                         (bases 1 to 2815)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:32493411
                                                                                                                                                              99 (26), 16899-16903 (2002)
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROD 10-JUL-2003
, mRNA (cDNA
                                                                                                                                                                                                                      full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus.
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                                                                                                                                                                     Query
                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                           US-10-659-004-104 (1-302) x BC054780
                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                       Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REMARK
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                                                                                                                                                                                                                                                                              No.:
                                                                                                                                                                        Match:
                                                                                                                                                                                                                                                                                                          Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: 0
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20982834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: bentō-soāres@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                           92 IleHisHisAspHisAspHisHisSerAspHisGluHisHisSerAspHisGluArgHis 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas L. Casavant.
Web site: http://genome.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product = "Ermelin-pending protein"
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EEPAMEMKGGTLFSHLSAQNIESSSFTWGGLTALGGLYFMFLVEHVLTLIKQFKD
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KKKKNQKKFENDEDVESKYGLSKYDSQLSNEEKVDFGERESYLRADSQEPSFDSQ
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                                                                                                                                                                                                                                                                                                                                                                                    SGLSTSVAVFCHELPHELGDFAVLLKAGMTVKQAVLYNALSAMLAYLGMATGIFIOHY
AENVSMMIFALTAGLFMYVALVDMVÞEMLHNDASDHGCSRWGYFFLQNAGILLGFGIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="LocusID:106957"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Ermelin-pending"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Ermelin-pending"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pYX-ASC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:10090"
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1002.00
92.89%
90.52%
62.66%
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                                                                                             (1-2815)
                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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CACATTCTGCAC 1181
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용 <i>성</i>	용 성	B 8	용 &	B 8	B 8	B 8	B 8	B 8	B 8
Qy 292 PheGluHisLysIleValPheArgIleAsnPhe 302	Qy 272 PhéPheLeuGlnAsnAlaGlyMetLeuLeuGlyPheGlyIleMetLeuLeuIleSeTIle 291	Qy 252 MetValProGluMetLeuHisAsnAspAlaSerAspHisGlyCysSerArgTrpGlyTyr 271	Qy 232 ValSerMetTrpIlePheAlaLeuThrAlaGlyLeuPheMetHisValAlaLeuValAsp 251	Qy 212 AlaMetLeuAlaTyrLeuGlyMetAlaThrGlyIleDheIleGlyHisTyrAlaGluAsn 231 	Qy 192 AlavalLeuLysAlaGlyMetThrValLysGlnAlaValLeuTyrAsnAlaLeuSer 211	Oy 172 GlyLeuSerThrSerValAlaValPheCysHisGluLeuProHisGluLeuGlyAspPhe 191	Oy 152 LeuHibabnPheSerAppGlyLeuAlaIleGlyAlaAlaPheThrGluGlyLeuSerSer 171	Qy 132 GluGluLeuLy8A8pAlaGlyValAlaThrLeuAlaTrpMetValIleMetGlyAspGly 151	Qy 112 SerAspHisGluHisHisSerAspHisHisProHisSerHisSerGlnArgTyrSerArg 131

Search completed: March 20, 2005, 00:33:45 Job time: 4947 secs

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Command line parameters:

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-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUPFIX=rng -MINMATCH=0.1 -LOOPCL=0
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-LIST=45 -DOCALICM=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQÜERY -NEGSCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                              Regult
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  1359.5
1359.5
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                                                                                                                              Score
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                                                                                                                                                                                                                                                                                                                N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001bs:*
5: geneseqn2002as:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
9: geneseqn2003bs:*
9: geneseqn2003bs:*
10: geneseqn2003bs:*
11: geneseqn2004bs:*
11: geneseqn2004as:*
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ALIGNMENTS

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AC ADL57158;
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18-MAR-2004 WO2004022723-A2

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The invention relates to a novel isolated polypeptide (NoVX) comprising a comparising a comparising and the form of any of the 37 amino acid sequences fully defined in the genetication. A polypeptide of the invention has antidabetic, cardiant, hypotensive, antiarteriosclerotic, ancrectic, cardiantic, and antiarteriosclerotic, cardiovascular diseases (hypertension, anterosclerosis), neurodegenerative disorders, lazheimer's chieferteriosion, anterosclerosis), neurodegenerative disorders, lazheimer's chieferteriosion, anterosclerosis, inclammatory skin disorders, costomatory skin disorders, antiarteriosclerosis, haematopoietic disorders, inflammatory skin disorders, costomatoriosclerosclerosclerosis, incurative disorders, lazheimer's chieferteriosclerosclerosis, haematopoietic, antiarterioscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleros
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12-SEP-2002; 2002US-04110320P.
16-SEP-2002; 2002US-0411060P.
23-SEP-2002; 2002US-0412766P.
23-SEP-2002; 2002US-0412765P.
24-SEP-2002; 2002US-0412767P.
24-SEP-2002; 2002US-0413342P.
Sequence 1101 BP;
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Alignment Scores:

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AsnPhe 302 AATTTC 102	LeuGlyPheG TTGGGTTTTG	AlaSerAspH GCTAGTGACC	AlaGlyLeuP GCTGGCTTAT	ThrGlyIleph	ValLysGlnA GTTAAGCAGG	CysHisGluLe	IleGlyAlaA ATTGGTGCTG	ThrLeuAlaT	HisProHisS CATCCTCACA	AspHisGluHi GACCACGAGCA	AsnileGlyI AATATAGGCA	PheTyrArg1	GluSerGlyI GAATCTGGCA	LeuHisGluL	MetAlaArgI ATGGCGAGGA	-104 (1-302	arity: milarity:
80		isGlyCysSerAr ATGGATGTAGCCG	heMetHisValAla "TCATGCATGTTGCT	helleGlyHisTyrA: TCATTGGTCATTATG	AlaValLeuTyrAsı GCTGTCCTTTATAA	uProHisGluI GCCTCATGAAI	aAlaPheThrGluGlyI GCTTTTACTGAAGGCT	.aTrpMetValIleMet(CTGGATGGTGATAATGC	RerHisSerGlnArg	sHisSerAspHi TCACTCAGACCA	leasplysilelys	TyrGlyGluAsnAsı TATGGAGAAATAA	leAsnValAspLe TTAATGTTGACTT	euLysAlaAlaAl TAAAAGCAGCTGO	;LysLeuSerVallle ;AAGTTATCTGTAATC) x ADL57158	2.31e-154 1599.00 100.00% 100.00% 100.00%
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	luHisLysIleValPheArgI 	LeuGlnasnalaGlyMetI TACAGAATGCTGGGATGC	.lProGluMetLeuHisAsnA ACCTGAAATGCTGCACAATG	erMetTrpIlePheAlaLeuTh ctatgtggatatttgcacttac	LeuAlaTyrLeuGlyMetA CTGGCGTATCTTGGAATGG	LLeuLeuLysAlaGlyMetTh TCTACTAAAGGCTGGCATGAC	uSerThrSerValAlaValPh AAGTACTTCTGTTGCTGTGTT	sAsnPheSerAspGlyLeuA CAATTTCAGCGATGGTCTAG	uLeuLysAspAlaGlyValA ctgaaagatgccggcgtcg	pHisGluHisHisSerAspH ccargagcarcactcagacc	sHisAspHisAspHisHisS CCATGACCACGACCATCACT	:luGlyPheArgLysLeuLeuG AAGGGTTCAGAAAATTACTTC	GGlnTyrHisLeuGlnGlnL GCAATATCATCTACAACAGC	rGluLy8IleSerProAsnTr TGAGAAAATTAGTCCGAATTG	rPheAlaLeuSerValThrAsnP CTTTGCCCTCTCTGTCACAAATC		1101 302 0
	le 300 TA 1022	eu 280	BP 260	hr 240 CT 842	la 220 CA 782	hr 200	he 180	la 160 CA 602	la 140 CC 542	is 120 AC 482	er 100 CA 422	1n 80 AA 362	eu 60	rp 40 GG 242	ro 20 CC 182		

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CC The invention relates to a novel isolated antibody or its antigen binding CC fragment that associates with either IGSF9 (immunoglobulin superfamily CC member 9) or LIV-1 polypeptide, and the fully defined polypeptides. The CC polypeptide comprises a sequence selected from ADR28009, ADR28012, ADR28012, ADR28028, ADR28029, ADR28031, and ADR28032, having CC officery and a partial for the invention further comprises: a composition CC comprising the antibody which associates with IGSF9 or LIV-1 for treating CC a neoplastic disorder or the polypeptide comprising the IGSF9 or LIV-1 for treating cancer comprising the IGSF9 or LIV-1 for treating cancer comprising the IGSF9 or LIV-1 for treating cancer in a native for treating cancer comprising the IGSF9 or LIV-1 for treating cancer comprising the IGSF9 or LIV-1 for treating cancer representation of IGSF9 or LIV-1 antigen or its fragment and a carrier; a method of coveracypression of IGSF9 or LIV-1 or its fragment and a carrier; a method of CC determining the prognosis of an individual receiving a cancer treatment; a method of IGSF9 or LIV-1 or its fragment; a method for creat comprising the composition together with instructions for use to consisting the concer; a method of treating a neoplastic disorder in a nucleotide portion of IGSF9 or LIV-1 which inhibits the expression of IGSF9 or LIV-1; a method of treating a neoplastic disorder in a nucleotide portion of IGSF9 or LIV-1 which inhibits the expression of IGSF9 or LIV-1; a method of inhibiting the expression of IGSF9 or LIV-1; a method of treating a pacted from the group consisting of: ADR28001, ADR28017, ADR28018, ADR28019, ADR28026; a vector comprising the nucleic acid; and a host cell comprising the concers in a nucleic acid; and a host cell comprising the concers in a nucleic acid; and a host cell comprising the concers in a nucleic acid; and a host cell comprising the concers in a nucleic acid; and a host cell comprising the concers in a nucleic acid; and a host cell comprising the concers in the concers in 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibody or its antigen binding fragment that associates with either IGSF9 or LIV-I polypeptide, and the polypeptides, useful in preparing a
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                                                    CCCCGAAAAGGCTTTATGTATTCCAGAAACACAAAATGAAAATCCTCAGGAGTGTTTCAAT
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The present invention describes a method for assessing whether a patient is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polypeptide see ACC50076 to ACC5034 and ABR47386 to ABR47632) in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level of expression of the marker in the facilities and the normal level is an indication that the patient is afflicted with breast cancer. The breast cancer associated sequences from the present invention have cytostatic activities and can be used in gene

Claim 1;

SEQ ID NO 263; 128pp; English

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27-JUN-2001;
18-JUL-2001;
25-SEP-2001;
                                                                                                      Breast cancer diagnosis or treatment of a marker in a patient sample with cancer sample.
                                                                                                                                                                                                                                                                                                                                                                          Breast
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14-MAY-2002;
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                                                                                                                                                                                                                      ; 2001US-0299887P.
; 2001US-0301572P.
; 2001US-0306501P.
; 2001US-0325002P.
; 2002US-0362585P.
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy. The method is useful for diagnosing and treating breast cancer. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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               GCATCAAAGCTACTGACATCTCATGGCATGGGCATCCAGGTTCCGCTGAATGCAACAGAG
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The invention relates to a method of classifying a cell sample as chronic phase chronic myelogenous leukaemia (CP-CML) or blast crisis CML (BC-CML). The method is useful for classifying a sample as CP-CML or BC-CML. The present sequence represents a human chronic myclogenous leukaemia (CML) gene marker used to distinguish blast crisis CML from chronic phase
                                                                                                                  Classifying cell sample as chronic phase chronic myelogenous leukemia blast crisis chronic myelogenous leukemia by detecting difference in expression of genes corresponding to the markers such as X15415, U894:
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MetTrpIlePheAlaLeuThrAlaGlyLeuPheMetHisValAlaLeuValAspMetVal
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                                          CTGGCGTATCTTGGAATGGCAACAGGAATTTTCATTGGTCATTATGCTGAAAATGTTTCT
                                                                         LeuAlaTyrLeuGlyMetAlaThrGlyIlePheIleGlyHisTyrAlaGluAsnValSer
                                                                                                                                    CTACTAAAGGCTGGCATGACCGTTAAGCAGGCTGTCCTTTATAATGCATTGTCAGCCATG
                                                                                                                                                                LeuLeuLysAlaGlyMetThrValLysGlnAlaValLeuTyrAsnAlaLeuSerAlaMet
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                                                                    US-10-659-004-104 (1-302) x ADN03826 (1-2744)
                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                 Sequence 2744 BP; 786 A; 585
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P-PSDB; ADN03827.
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27-DEC-2002;
25-APR-2003;
28-APR-2003;
21-OCT-2003;
22-OCT-2003;
                                                                                                                                       The invention relates to purified proteins and genes encoding them, that are involved in T cell activation (I) and has an amino acid deletion, substitution or addition in the amino acid sequences. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of autoimmune disease (rheumatoid arthritis, asthma, multiple sclerosis and diabetes), allergic disease, infectious disease, ADDS, and acute or chronic rejection at organ transplant or bone marrow transplant. This sequence corresponds to a cDNA for a protein involved in T cell activation.
                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                   New purified protein involved in T cell activation, useful for diagnosing, preventing and/or treating acquired immunodeficiency syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), and infectious diseases.
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anti-HIV; antimicrobial; antirheumatic; immunosuppressive;
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; 2002JS-0436473P.
; 2003JP-00122113.
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LeuGlnAsnAlaGlyMetLeuLeuGlyPheGlyIleMetLeuLeuIleSerIlePheGlu
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MetAlaArgLysLeuSerVallleLeuIleLeuThrPheAlaLeuSerValThrAsnPro

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:

3.19e-129 1359.50 40.32% 40.19% 85.02%

> Length: Matches: Conservative:

> > 2744 301

Alignment Scores: Pred. No.:

US-10-659-004-104 (1-302) x ADR25539

(1-2744)

Mismatches: Indels: Gaps:

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                                                            The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
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Alignment Scores:
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                                                                                                                                                        CC angiogenesis and cell remodelling. The structure of LIV-1 implicates a C role for the protein as a zinc-influx transporter protein. LIV-1 cd distribution studies indicate primary expression in breast, prostate, CC pituitary gland and brain tissue. This protein has also been implicated in certain cancerous conditions like breast cancer, prostate cancer and CC colorectal carcinoma. The antibody used in the invention is conjugated to a cytocoxic chemical. The cytocoxic chemical is auxistatin-E. Treating CC an individual with prostate or breast cancer comprises administering the CC above antibody or double-stranded ribonucleic acid. The antibody is a monoclonal antibody, an antibody fragment, or a humanized antibody. The convention also provides double-stranded ribonucleic acids that bind to CC mRNA encoded by the LIV-1 nucleic acid. These mRNA molecules can be used as cytocoxic agent for LIV-1 expressing cells. LIV-1 has been CC as a cytocoxic agent for LIV-1 expressing cells. LIV-1 has been contained the contained contained and lobular carcinoma contained the breast, epithelial neoplasma, small cell tumous and germ cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses antibodies that specifically bind to LIV-1 protein which can be used for diagnosis, prognosis, and therapy of cancer. LIV-1 is a member of the LZT (LIV-1-ZIP Zinc transporters subfamily of zinc transporter proteins. Zinc plays an essential role in cell growth and is a cofactor of over 300 enzymes, including enzymes important in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New anti-LIV-1 antibodies that specifically bind to LIV-1 proteins, useful for diagnosing, prognosing or treating cancer, particularly
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The present invention describes an isolated PRO nucleic acid (I). Also c described: (I) a vector comprising (I); (2) a host cell comprising the vector of (I); (3) a process for producing a PRO polypeptides; (4) an c isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) fused to a heterologous amino acid sequence; (6) an c antibody which specifically binds to a polypeptide of (4); (7) a c composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a container of (7); (9) a method of treating an immune related disease in a container and a composition of container and a composition of container and a composition of container of (7); (9) a method of treating an immune related disease in a container and a composition of container and a	Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM; Wood WI, Wu TD; WPI; 2004-376182/35. P-PSDB; ADP56128. New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.	n; PRO; immune response st asthmatic; ant trheumatic; hepat rotropic; neur cide; gene the sapiens. 04039956-A2. AY-2004. CT-2003; 2003W	T 9 127 ADP56127 standard; cDNA; 2744 BP. ADP56127; 18-NOV-2004 (first entry) Human PRO cDNA sequence SEQ ID NO:2103.	294 HisLysileValPheArgIleAsnPhe 302 	274 LeuGlnAsnAlaGlyMetLeuLeuGlyPheGlyIleMetLeuLeuIleSerIlePheGlu 293 	2238 CCTGAAATGCTGCACAATGATGCTAGTGACCATGGATGTAGCCGCTGGGGGTATTTCTTT 2297

The present invention describes an isolated PRO nucleic acid (I). Also CC described: (I) a vector comprising (I); (2) a host cell comprising the CC vector of (I); (3) a process for producing a PRO polypeptides; (4) an CC isolated PRO polypeptide; (5) a chimeric molecule comprising the CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an CC antibody which specifically binds to a polypeptide of (4); (7) a CC composition of matter comprising a polypeptide of (4), an agonist or CC antagonist of the polypeptide or an antibody that binds to the comprising a container, a label on the container and a composition of CC comprising a container, a label on the container and a composition of CC matter of (7); (9) a method of treating an immune related disease in a sample suspected of having the presence of a PRO polypeptide CC diagnosing an immune related disease or an inflammatory immune response in a mammal; (12) a method of identifying a compound that inhibits or CC mimics the activity of or expression of a gene encoding a PRO polypeptide; and (13) a method of stimulating the immune response in a memmal. The CC antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic,

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174 SerThrSerValAlaValPheCysHisGluLeuProHisGluLeuGlyAspPheAlaVal 193	AATTTCAGCGATGGCCTAGCAATTGGTGCTGCTTTTACTGAAGGCTTATCAAGTGGTTTA	AsnPheSerAsnGlvI.euAlaIleGlvAlaAlaPheGluGlvI.euSerSerGlvI.eu	1940	CAICACCACCAMANCCACCAICCICACAGICACAGICACGIACICICGGAAGGAG	H18H18ProH18SerH18SerG1nArgTyrSerArgG1uG1u	ACACTCGGCCAGTCAGACGATCTCACCACCATCATGACTACCATCATATTCTCCAT		GTCTACAATGAATAIGTACCCAGAGGGTGCAAGAATAAATGCCATTCACATTTCCACGAT		CAGCAGCCTGCAGTCTTGGAAGAAGAAGAGGTCATGATAGCTCATGCTCATCCACAGGAA	119 119	1578 GATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAGCCCTCCCACTTTGATTCT 1637	119 119	1518 AAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAATGAGGAGAAAGTAGATACA 1577	119 119	1458 TTTAAAGATAAGAAAAAAGAATCAGAAGAAACCTGAAAATGATGATGATGTGGAGATT 1517	119 119	1398 GCTCTAGGAGGCCTGTATTTCATGTTTCTTGTTGAACATGTCCTCACATTGATCAAACAA 1457	119 119	1338 CTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCCACGTGGAAGGGTCTAACA 1397	119 119	1278 CATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGAGGACCACTTTTCAGTCAT 1337	119 119	1218 GGGACTTTGAGTGGTGATGCTTTTTTACACCTTCTTCCACATTCTCATGCAAGTCACCAC 1277	119 119	1158 CCTCTCATGAATCGGGTGTTTTTCAAATTTCTCCTGAGTTTCCTTGTGGCACTGGCCGTT 1217	119 119	1098 GGTGGTTTTATAGCCATTTCCATCATCAGTTTCCTGTCTCTGCTGGGGGTTATCTTAGTG 1157	119 119	1038 ACAAGTGAAAAGAAGGCTGAAATCCCCTCCAAAGACCTATTCATTACAAATAGCCTGGGTT 1097	119 119	978 TICAACTATCTCTGTCCAGCCATCATCAACCAAATTGATGCTAGATCTTGTCTGATTCAT 1037	119 119	918 GCATCAAAGCTACTGACATCTCATGGCATGGGCATCCAGGTTCCGCTGAATGCAACAGAG 977	119 119

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Schmitt A
This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in
                                                                                                                                                  useful
                                                                                                                                                                     New nucleic
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(ROSE/)
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PILARSKY C.
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ROSENTHAL A.
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Beckmann
Staub E;
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orf T, Kinnemann H, Roe
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CC prostatic tissue. Screening for inhibitors of the sequences or detection CC substances involves a binding assay, any compounds that bind are CC selected, optionally after deconvolution of mixtures. Detection of a CC predetermined minimum level of the reporter indicates the presence of CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides, CC short-interfering RNA or ribozymes; an organic molecule of molecular CC weight below 5000, preferably 300, that binds to the polypeptide; an CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the CC polypeptide, preferably humanised or human; an anti-idiotype, non-human CC (monoclonal) antibody directed against Ab or any of the above derivatised CC with a reporter group, cell toxin, immunostimulatory molecules and/or CC radioisocope. The polymucleotides are identified in human prostatic C cancer by differential expression nanlysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that C complex this cancer patients, or subjects at risk, were incubated complex were counterstained with hemalum (blue). Malignant cells stained CC biotinylated second antibody; streptavidin-conjugated horseradish CC biotinylated second antibody; streptavidin-conjugated horseradish CC samples were counterstained with hemalum (blue). Malignant cells stained CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and CC polymucleotide and polypeptide sequences used in the method of the CC invention.

Sequence 2744 BP; 786 A; 585 C; 601 G; 772 T; 0 U; 0 Other;

Best Local Similarity: Query Match: DB: US-10-659-004-104 (1-302) x ADR66497 Percent Similarity: Alignment Scores: Pred. No.: 498 438 101 378 318 258 198 138 81 61 41 21 AspHisGluHisHisSerAspHisGluArgHisSerAspHisGluHisHisSerAsp---AsnIleGlyIleAspLysIleLysArgIleHisIleHisHisAspHisAspHisHisSer GAATCTGGCATTAATGTTGACTTGGCAATTTCCACACGGCAATATCATCTACAACAGCTT GluSerGlyIleAsnValAspLeuAlaIleSerThrArgGlnTyrHisLeuGlnGlnLeu LeuHisGluLeuLysAlaAlaAlaPheProGlnThrThrGluLysIleSerProAsnTrp ATGGCGAGGAAGTTATCTGTAATCTTGATCCTGACCTTTTGCCCTCTCT MetAlaArgLysLeuSerValIleLeuIleLeuThrPheAlaLeuSerValThrAsnPro GACCACGAGCATCACTCAGACCATGAGCGTCACTCAGACCATGAGCATCACTCAGACCAC AATATAGGCATAGATAAAGATTAAAAGAATCCATATACACCATGACCACGACCATCACTCA PheTyrArgTyrGlyGluAsnAsnSerLeuSerValGluGlyPheArgLysLeuLeuGln CTTCATGAACTAAAAGCAGCTGCTTTCCCCCCAGACCACTGAGAAAATTAGTCCGAATTGG CCAGACCATGACTCAGATAGTTCAGGTAAAGATCCTAGAAACAGCCAGGGGAAAGGAGCT GAGCATCACTCTGACCATAATCATGCTGCTTCTGGTAAAAATAAGCGAAAAAGCTCTTTGC TTCTACCGCTATGGAGAAAATAATTCTTTGTCAGTTGAAGGGTTCAGAAAATTACTTCAA 1359.50 40.32% 40.19% 85.02% 3.19e-129 (1-2744)Length:
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(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
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14-MAY-2003;
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25-MAY-2000; 2
09-JUN-2000; 2
18-JUL-2000; 2
13-DEC-2000; 2
                                                                                                                                                                                                                                                                                                                                                                               Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, uses
                                                                                                                                                                                        WPI, 2001-662795/76:
                                                                                                                                                    for detecting presence of prostate cancer, stage of prostate
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; 2000US-0255281P.
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate call carcinogenic potential of a compound; (g) assessing the aggressiveness or indolence of prostate cancer in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker Claim 1; Page 5169-5170; 11750pp; English.

Score: Alignment Sequence 3523 No.: Scores: BP; 1071 A; 684 C; 4.49e-129 1359.50 40.32% 40.19% 85.02% Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 735 G; 1013 T; 0 U; 20 Other; 3523 301 1 0 447

US-10-659-004-104 (1-302) x ABV25747 (1-3523)

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                                                                                                                                                                   CTTCATGAACTAAAAGCAGCTGCTTTCCCCCCAGACCACTGAGAAAATTAGTCCGAATTGG
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AsnIleGlyIleAspLysIleLysArgIleHisIleHisHisAspHisAspHisHisSer
                                                                        PheTyrArgTyrGlyGluAsnAsnSerLeuSerValGluGlyPheArgLysLeuLeuGln
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AspHisGolimisHisSerAspHisGoluArgHisGoluHisHisGoluHisHisGoluHisHisGoluHisHisGoluHisHisGoluHisHisGoluHisHisGoluHisHisGoluHisHisGoluHisHisHisHisHisHisHisHisHisHisHisHisHisH	?`}	CCCCGAAAAGGCTTTATGTATTCCAGAAACACAAATGAAAATCCTCAGGAGTGTTTCAAT 917
ABPHIRESCALIAGE APPROPRIATE CONTROL APPROPRIATE CONTROL APPRICATION CONTROL AP	Z-2	119
ABPHI SCILLIANS LANGE		ACATCAAAGAGCCGGGTGAGCCGGCTGGCTGGTAGGAAAACAAATGAATCTGTGAGTGA
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AppHisGluHisHisSerAspHisGluArgHisSerAspHisGluHisHisSerAsp 119	ACACTCGGCCAGTCAGAC	GTGACCTCAACTGTGTACAACACTGTCTCTGAAGGAACTCACTTTCTAGAGACAATAGAG 737
AspHisGluHisHisSerAspHisGluArgHisSerAspHisGluHisHisSerAsp 119	- 1	119
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78831-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCAGCCTGCAGTCTTGGAAGAAGAAGAGGTCATGATAGCTCATGCTCATCCACAGGAA 1697
                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGAAATGCTGCACAATGATGCTAGTGACCATGGATGTAGCCGCTGGGGGGTATTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACACTCGGCCAGTCAGACGATCTCATTCACCACCATCATGACTACCATCATATTCTCCAT 1817
                                                                                                                                                                                      (first
                                                                                                                               cancer;
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                                                                                                                                                                                                                                               CDNA;
                                                                                                                                                                                      entry)
                                                                                                                               cytostatic;
                                                                                                                                                                                                                                                 2268
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                                                                                                                                                                                                                                               ВÞ
                                                                                                                                                           cDNA sequence SEQ
                                                                                                                               gene
                                                                                                                               therapy; vaccine; gene;
                                                                                                                                                           ID NO:176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for detecting a bladder cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridises to a sequence that is 80 % identical to a
CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications
                                                                                                                                                                                                                                                                                                                                                                                           US-10-659-004-104 (1-302) x ACC51044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
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03-AUG-2001;
08-NOV-2001;
13-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a bladder cancer-associated transcript in a cell patient, comprises contacting a biological sample from the bladder cancer-associated polynucleotide or antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patient, comprises contact bladder cancer-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 290; 307pp; English.
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DB; ABR48228.
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                                                                                                                                                                                                                                                                                            LeuHisGluLeuLysAlaAlaAlaPheProGlnThrThrGluLysIleSerProAsnTrp
                                                                                                                                                                                                                                                                                                                                   ATGGCGAGGAAGTTATCTGTAATCTTGATCCTGACCTTTGCCCCTCTCTGTCACAAATCCC
                                                                                                                                                                                                                    GAATCTGGCATTAATGTTGACTTGGCAATTTCCACACGGCAATATCATCTACAACAGCTT
                                                                                                                                                                                                                                                                             CTTCATGAACTAAAAGCAGCTGCTTTCCCCCCAGACCACTGAGAAAATTAGTCCGAATTGG
                                                                                                                                                                                                                                                                                                                                                    MetAlaArgLysLeuSerValIleLeuIleLeuThrPheAlaLeuSerValThrAsnPro
                                                                AspHisGluHisHisSerAspHisGluArgHisSerAspHisGluHisHisSerAsp---
                                                                                                    PATATAGGCATAGATAAGATTAAAAGATCCATATACACCATGACCACGACCATCACTCA
                                                                                                                      AsnIleGlyIleAspLysIleLysArgIleHisIleHisHisAspHisAspHisHisSer
                                                                                                                                                                          PheTyrArgTyrG1yG1uAsnAsnSerLeuSerValG1uG1yPheArgLysLeuLeuG1n
                                            GACCACGAGCATCACTCAGACCATGAGCGTCACTCAGACCATGAGCATCACTCAGACCAC
                                                                                                                                                             TTCTACCGCTATGGAGAAAATAATTCTTTGTCAGTTGAAGGGTTCAGAAAATTACTTCAA
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2001US-0310099P.
2001US-0343705P.
2001US-0350666P.
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1356.50
40.00%
39.87%
84.83%
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Matches:
Conservative:
Mismatches:
Indels:
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119 300 240 80 180

KW alpha-2 mac	1441 GAGGAGAAAGTAGATACAGATGATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAG 1500	뮍
KW MDC3; T-lym	119 119	Ş
KW fibroblast	1381 GATGATGATGTGGAGATTAAGAAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAAT 1440	b
KW anticonvuls	119 119	Ş
KW antiarterio	1321 CTCACATTGATCAAACAATTTAAAGATAAGAAGAAAAAGAATCAGAAGAAACCTGAAAAT 1380	망
XX XX AG. CORO. h	119 119	Ş
XX XX Himan NOV9A	1261 ACGTGGAAGGGTCTAACAGCTCTAGGAGGCCTGTATTTCATGTTTCTTGTTGAACATGTC 1320	В
XX	119 119	ş
XX ADLETIED.	1201 GGACCACTTTTCAGTCATCTGTCTTCTCAAAACATAGAAGAAAGTGCCTATTTTGATTCC 1260	Db
7160	119 119	Ş
. 444	1141 TCTCATGCAAGTCACCACCATAGTCATAGCCATGAAGAACCAGCAATGGAAATGAAAAGA 1200	₽
	119 119	Ş
) H	1081 CTTGTGGCACTGGCCGTTGGGACTTTGAGTGGTGATGCTTTTTTACACCTTCTTCCACAT 1140	망
.	119 119	Ş
896	1021 CTGGGGGTTATCTTAGTGCCTCTCATGAATCGGGTGTTTTTCAAATTTCTCCTGAGTTTC 1080	Вb
3 101	119 119	Ş
248	961 TTACAAATAGCCTGGGTTGGTGGTTTTATAGCCATTTCCATCATCAGTTTCCTGTCTCTG 1020	망
Db 2041 TA	119 119	ş
) i	901 AGATCTTGTCTGATTCATACAAGTGAAAAGAAGGCTGAAAATCCCTCCAAAGACCTATTCA 960	8
	119 119	Ş
202	841 CCGCTGAATGCAACAGAGTTCAACTATCTCTGTCCAGCCATCATCAACCAAATTGATGCT 900	В
	119 119	Ş
188	781 CCTCAGGAGTGTTTCAATGCATCAAAGCTACTGACATCTCATGGCATGGGCATCCAGGTT 840	망
1861	119 119	Ş
168	721 AATGAATCTGTGAGTGAGCCCCGAAAAGGCTTTATGTATTCCAGAAACACAAATGAAAAT 780	맑
Dh 1801 AT	119 119	Ş
1471	661 TCCACTCCACCCAGTGTCACATCAAAGAGCCGGGTGAGCCGGCTGGCT	망
1741	119 119	Ş
100	601 TTTCTAGAGACAATAGAGACTCCAAGACCTGGAAAACTCTTCCCCCAAAGATGTAAGCAGC 660	망
1601	119 119	ફ
	541 AGTGTTAGTGCTAGTGAAGTGACCTCAACTGTGTACAACACTGTCTCTGAAGGAACTCAC 600	뭥
Db 1621 Ca	119 119	ş
110	481 AGCCAGGGGAAAGGAGCTCACCGACCAGAACATGCCAGTGGTAGAAGGAATGTCAAGGAC 540	₽
1561	119 119	Ś
119	421 AAGCGAAAAGCTCTTTGCCCCAGACCATGACTCAGATAGTTCAGGTAAAGATCCTAGAAAC 480	몽
1501	119 119	Ş
Oy 119	361 GAGCATCACTCTGACCATGATCATCACTCCCACCATAATCATGCTGCTTCTGGTAAAAAT 420	D

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snAlaLeuSerAlaMetLeuAláTyrLeuGlyMetAlaThrGlyIlePheIleGlyHis 227
      tandard;
                                                                                                                                                              eulleSerIlePheGluHisLysIleValPheArgIleAsnPhe 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTGGTTGATATGGTACCTGAAATGCTGCACAATGATGCTAGTGACCATGGATGTAGC 2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euGlyAspPheAlaValLeuLeuLysAlaGlyMetThrValLysGlnAlaValLeuTyr 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTCACATTTCCACGATACACTCGGCCAGTCAGACGATCTCATTCACCACCATCATGAC 1680
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                                                                                                                                                                                                                                                     GCTGGGGGTATTTCTTTTTACAGAATGCTGGGATGCTTTTGGGTTTTTGGAATTATGTTA 2220
                                                                                                                                                                                                                                                                                     rgTrpGlyTyrPhePheLeuGlnAsnAlaGlyMetLeuLeuGlyPheGlyIleMetLeu 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGCATTGTCAGCCATGCTGGCGTATCTTGGAATGGCAACAGGAATTTTCATTGGTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rgTyrSerArgGluGluLeuLygAspAlaGlyValAlaThrLeuAlaTrpMetValIle 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTCCCACTTTGATTCTCAGCAGCCTGCAGTCTTGGAAGAAGAAGAAGAGGTCATGATAGCT 1560
                                                                                                                             TATTTCCATATTTGAACATAAAATCGTGTTTCGTATAAATTTC 2265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rAlaGluAsnValSerMetTrpIlePheAlaLeuThrAlaGlyLeuPheMetHisVal 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLeuSerSerGlyLeuSerThrSerValAlaValPheCysHisGluLeuProHisGlu 187
                                                                                                                                                                                                                                                                                                                                                                                                                aLeuValAspMetValProGluMetLeuHisAsnAspAlaSerAspHisGlyCysSer 267
DNA; 2268
   BP.
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gene SEQ ID NO:105. (first entry)

human; antidiabetic; amorectic; cardiant; hypotensive; iosclerotic; anorectic; virucide; antibacterial; fungicide; ide; mootropic; neuroprotective; antiparkinsonian; leant; osteopathic; antiarthritic; antiinflammatory; gical; antiasthmatic; antilipaemic; gene therapy; t growth factor receptor 4; FGFR4; t factor precursor; matrix metalloproteinase-15 precursor; ymphocyte surface antigen Ly-9 precursor; t growth factor-21; FGF-21; t growth factor-21; FGF-21;

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CC virucide, antibacterial, fungicide, protozoacide, nootropic, antibacterial, fungicide, protozoacide, nootropic, antibacterial, fungicide, protozoacide, nootropic, and convulsant, anticonvulsant, osteopathic, and cativity. A polymucleotide of the invention may have a use can gene therapy. The polypeptides, nucleic acid molecules and antibodies casociated with a human disease, preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful in the manufacture of a medicament for treating a syndrome casociated with a human disease, preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as metabolic disorders, catality, and protozoal), anorexia, cancer, cardiovascular diseases (harkinson's disease, epilepsy, immune disorders (hypertension, atherosclarosis), neurodegenerative disorders (hypertension, haematopoletic disorders, inflammatory skin disorders, castima, and various dyslipidaemias. The nucleic acids and polypeptides con that modulate or inhibit e.g. neurogenesis, cell differentiation, cell cristue typing, preventive metiodies that bind immunospecifically to NOVX calls are further used as hybridisation probes, in chromosome mapping, citseus typing, preventive medicine, and pharmacogenomics. The nucleic acids are further used as hybridisation probes, in chromosome mapping, convertions; novica shows homology to estatin known human (convertions) notes; novica show homology to fibroblast growth factor receptor 4 (FGRA4), NOV2a shows homology to fibroblast growth factor 1000 and convertion show homology to T-lymphocyte surface antigen convertion to the convertion of antigenest factor in growth factor—21 (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like colypeptide variant; NOV8a-8g show homology to antileukoproteinase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-SEP-2002;
23-SEP-2002;
24-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated polypeptide (NOVX) compr mature form of any of the 37 amino acid sequences fully defined in specification. A polypeptide of the invention has antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated NOVX polypeptides and polynu preventing, diagnosing or treating NOVX-a osteoarthritis, obesity, atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma, or infections
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12-SEP-2002;
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2002US-0410320P.
2002US-0411060P.
2002US-0412766P.
2002US-0412825P.
2002US-0412825P.
2002US-0412825P.
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2002US-0414832P.
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ALIGNMENTS

PUBMED REFERENCE AUTHORS REFERENCE AUTHORS TITLE JOURNAL MEDLINE ACCESSION VERSION KEYWORDS SOURCE RESULT 1 AK028976 REFERENCE DEFINITION rocus JOURNAL MEDLINE PUBMED AUTHORS TITLE ORGANISM Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P. Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., AKU28976

3834 bp mRNA linear HTC 03-APR-2000-Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone-4732477B07 product:ESTROGEN REGULATED LIV-1 PROTEIN homolog [Homo sapiens], full insert sequence. Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus AK028976 20499374 AK028976.1 GI:26324937 11042159 L0349636 Carninci, P., genes

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Direct Submission

AL Direct Submission

AL Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.jp, Tax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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6 (bases 1 to 3834)
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URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Please visit our web site for further details.
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HHHDYHHILHHHHONHHBHSGRKYBEELKDAGIATLAWMVIMGDGLHHFSDGLAI
GAAFTEGLSSGLSTSVAVFCHELPHELGDFAVLLKAGMTVKQAVLYNALSAMLAYLGM
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                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Kristi A. Egland, Ira Pastan

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection Unpublished (1999)
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                                                                                                                                                                                                                             quality sequence stop:
                                                                                    /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6721115"
/cell line="ZR-75-1, MCF7,
hTERT-HME1, LNCAP"
/clone lib="MAPCL"
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
                                                                                                                                                                                                             ocation/Qualifiers
                                                                        lab_host="EMDH10B"
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Catarrhini; Hominidae;
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sapiens cDNA clone IMAGE:6721115 5',
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                                                                 AGENCOURT 14214060 NIH NIMAGE:30385255 5', mRNA CD251026 CD251026.1 GI:31011492
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          Homo sapiens
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                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisHisSerAspHisGluArgHisSerAspHisGluHisHisSerAspHisHisProHis 123
                                                                                                                                                                              GGAATTATGTTACTTATTTCCATATTTGAACATAAAATCGTGTTTCGTATAAATTTC
                                                                                                                                                                                             GlyIleMetLeuLeuIleSerIlePheGluHi8Ly8IleValPheArgIleAsnPhe
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A sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC Clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov Blate: NDAM452 row: a column: 08
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Tissue Procurement: Dr. Michael Brownstein
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                     AlaValLeuTyrAsnAlaLeuSerAlaMetLeuAlaTyrLeuGlyMetAlaThrGlyIle 223
                                                                                             LeuProHisGluLeuGlyAspPheAlaValLeuLeuLysAlaGlyMetThrValLysGln
                                                                                                                                               GCTTTTACTGAAGGCTTATCAAGTGGTTTAAGTACTTCTGTTGCTGTGTTCTGTCATGAG
                                                                                                                                                                     AlaPheThrGluGlyLeuSerSerGlyLeuSerThrSerValAlaValPheCysHisGlu 183
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GCTGTCCTTTATAATGCATTGTCAGCCATGCTGGCGTATCTTGGAATGGCAACAGGAATT
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/lab host="PHIOB-Ton A (T1 and T5 phage resistances)"
/clone lib="NIH_MGC 179"
/clone lib="NIH_MGC 179"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: EcoRV (destroyed); Site_2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Uni
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 756)
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              /organism="Mus musculus"
/mol_type="mRNA"
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Mammalia; Butheria; Primates; Catarrhini; H
1 (bases 1 to 906)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Ge
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                     906 bp mRNA linear EST 13-SEP-2002
AGENCOURT_10325419 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6573733
5', mRNA sequence.
BU541953
                                                                                                                                                           TSE
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                        BU541953.1 GI:22852436
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2767 row: o column: 13
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PheMetHisValAlaLeuValAspMetValProGluMetLeuHisAsnAspAlaSerAsp
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Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
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/db_xref="taxon:9606"
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UI-R-CX08-ccs-f-08-0-UI.sl UI-R-CX08 Rattus
UI-R-CX08-ccs-f-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
non-normalized rat placenta pool library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 565-605,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Iowa
375 Newton Road , 4156
Tel: 319 335 8250
Fax: 319 335 9565
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Mammalia; Eutheria;
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//lab host="DHI/OB [Life Technologies]"

//lab host="DHI/OB [Life Technologies]"

//clome lib="UI-R-CXOS"

//clome lib="UI-R-CXOS"

//clome lib="UI-R-CXOS"

//clome lib="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CXOS library is a non-normalized library constructed from the following rat placenta tissues: embryonic day 17, embryonic day 19, embryonic day 21. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research control of the library control of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research control of the library constructed from the following control of the library constructed from the library constructed from the following control of the library constructed from the following control of the library constructed from the following control of the library constructed from the library constructed from the following control of the library constructed from the following control of the library constructed from the library con
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TAG_TISSUE=rat placenta pool TAG_LIB=UI-R-CX08
                                                                                6:791-806, 1996)
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/clone="UI-R-CX0s-ccs-f-08-0-UI"
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Piao; Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA librar.
submicrogram amounts of total RNAs by a universal PCI
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              11544199
Contact: Dawood B. Dudekula
 Laboratory of Genetics
                                          21429098
                                                     Genome Res. 11
                                                                                                                                                              Mus musculus
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Lim,M.K. and Ko,M.S.H.
cong-transcript enriched cDNA libraries
ong-f total RNAs by a universal PCR an
                                                     1553-1558
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100.00%
98.36%
59.29%
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(1-665)

GCTGTTTTGCTAAAGGCTGGCATG

219 241 199 181 179

121

159 61 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U Email: cdnaelgsun.grc.nia.nih.gov
Plate: A0539 row: C column: 05
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5'-PGACTAGATCGTAGATCGCGAGCGCCCTTTTTTTTTTT-3'] from 2.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sall; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 153-1558 (2001). [PMD: 11544199]). Total RNAs were obtained from Dr. Akhiro Umezawa (Keio University School of Medicine, Japan). Double-stranded cDNAs were synthesized with an Oligo(dT) primer
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/mol type="mRNA"
/strain="C3H/He mice"
/db_xref="nilaEST:A0539C05-5"
/db_xref="taxon:10090"
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/lab_host="DH10B"
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                                                                                                              No.:
                                                                                                                                Scores:
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Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequrefegenoscope.cns.fr, Web: www.genoscope.cns.fr
Est strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length CDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BX327149
BX327149 Homo sapiens PLACENTA COT 25-NORMALIZED Clone CSODIO23YO21 5-PRIME, MRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.genoscope.cns.fr/cdna?s=CSOBAF023ZD10_AF02189_1&c=8883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
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                                                                                                                                                                                  /tissue_type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                 found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM14282 row: i column: 11
                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland,
                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini
(bases 1 to 893)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                     cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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582 k
BP259977 Sugano cDNA library,
HRT08420, mRNA sequence.
BP259977
BP259977.1 GI:52175207
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                                                                                                                                       LeuLeuIleSerIlePheGluHisLysIleValPheArgIleAsnPhe 302
                                                                                                                                                                                                  SerArgTrpGlyTyrPhePheLeuGlnAsnAlaGlyMetLeuLeuGlyPheGlyIleMet
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/mol types"mRNA"
/mol types"mRNA"
/db_xrefs"taxon:9606"
/db_xrefs"taxon:9606"
/clones"IMAGE:6721427"
/clones"IMAGE:6721427"
/clones"IMAGE:75-1, MCF7, SK-BR-3, MDA-MB-231,
hTERT-HMEI, LNCap"
/lab_host="MAPCL"
/lab_host="MAPCL"
/notes"Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
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Qy 2 рь 4	Оу 2 Db 4	Qy 2	Qy 2 Db 3	Qy 2 Db 2	Qy 1 Db 1	Qy 1 Db 1	Db 1	Qy 1 Db	US-10-659-0	Alignment S Pred. No.: Score: Score: Percent Sim Best Local Query Match DB:	FEATURES SOUTCE	JOURNAL COMMENT	TITLE	REFERENCE	SOURCE ORGANISM
284 GlylleMetLeuIeuIleSerIlePheGluHisLysIleValPheArgIleAsnPhe 302	264 HisGlyCysSerArgTrpGlyTyrPhePheLeuGlnAsnAlaGlyMetLeuLeuGlyPhe 283	244 PheMetHisValAlaLeuValAspMetValProGluMetLeuHisAsnAspAlaSerAsp 263 ::	224 PhelleGlyHisTyrAlaGluAsnValSerMetTrpllePheAlaLeuThrAlaGlyLeu 243 	204 AlaValLeuTyrAsnAlaLeuSerAlaMetLeuAlaTyrLeuGlyMetAlaThrGlyIle 223 	184 LeuProHisGluLeuGlyAspPheAlaValLeuLeuLysAlaGlyMetThrValLysGln 203	164 AlaPheThrGluGlyLeuSerSerGlyLeuSerThrSerValAlaValPheCysHisGlu 183 	144 TrpMetVallleMetGlyAspGlyLeuHisAsnPheSerAspGlyLeuAlaIleGlyAla 163 	124 SerHisSerGInArgTyrSerArgGluGluLeuLysAspAlaGlyValAlaThrLeuAla 143 	004-104 (1-302) x BP259977 (1-582)	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: S5.85% Gaps: Length: Matches: 177 Matches: 177 Mismatches: Indels: Gaps: Gaps: O	Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp. Location/Qualifiers 1. 582 /organism="Homo sapiens" /mol type="mRNA" /db xref="taxon:9606" /clone="HRT08420" /tissue type="heart" /tissue type="heart" /clone_Tib="Sugano cDNA library, heart"	Genome Res. 14 (9), 1711-1718 (2004) Contact: Yutaka Suzuki Department of Virology	reals a hom	Bukaryota; metazoa; Chordata; tranlata; vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 582) Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,	Homo sapiens (human)

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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Department of Biomolecular Sciences
University of Manchester Institute of Science
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                               AgpAlaGlyValAlaThrLeuAlaTrpMetValIleMetGlyAspGlyLeuHisAsnPhe
                                                                                            CATCATCAGAACCATCATCCACACACACAGTCAGCGCTACTCGCGTGAAGAACTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="CSEQRBN22"
/clone lib="CSEQRBN22"
/note="Vector: pBluescript II KS(+); Site 1: EcoRI;
/note="Vector: pBluescript II KS(+); Site 2: NotI; rhis first strand in Independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
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/mol_type="mRNA"
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db_xref="taxon:9031"
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97.24%
92.82%
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_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Ir
cDNA Library Preparation: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 791)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCML542 row: p column: 18
High quality sequence stop: 633.
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EST.
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602575672F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703873 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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/clone="IMAGE:4703873"
/lab host="PH108 (TI phage-resistant)"
/lab host="PH108 (TI phage-resistant)"
/clone lib="NIH MGC 77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgcctcggcc); Site_2: SfiI (ggcattateggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCCC-3' and 3' adaptor sequence:
g'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                   ocation/Qualifiers
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Average insert size 1.9

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RESULT 13
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                                                                                                                                           S39 bp
NISC gl07g06.yl NCI_CGAP_Lei2 Homo
5, mRNA sequence.
CB052402
CB052402.1 GI:27790689
EST.
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation:
                                                         Mammalia, Eutheria, Primates, Catarrhini, Hon
1 (bases 1 to 539)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                        Eukaryota; Metazoa;
                                                                                                                     Homo
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875.00
99.42%
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54.72%
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Primates;
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US-10-659-004-104 (1-302) x CB052402
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Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
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Plate: LLAM8057 rov
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                                                                                                                         MetLeuHisAsnAspAlaSerAspHisGlyCysSerArgTrpGlyTyrPhePheLeuGln
IleValPheArgIleAsnPhe 302
                                                         AsnAlaGlyMetLeuLeuGlyPheGlyIleMetLeuLeuIleSerIlePheGluHisLys
                                                                                                                                                                     LysAlaGlyMetThrValLysGlnAlaValLeuTyrAsnAlaLeuSerAlaMetLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerAspGlyLeuAlaIleGlyAlaAlaPheThrGluGlyLeuSerSerGlyLeuSerThr 175
                                        AATGCTGGGATGCTTTTGGGTTTTTGGAATTATGTTACTTATTTCCATATTTGAACATAAA
                                                                                                        ATGCTGCACAATGATGCTAGTGACCATGGATGTAGCCGCTGGGGGTATTTCTTTTTACAG
                                                                                                                                                                                                                                      TATCTTGGAATGGCAACAGGAATTTTCATTGGTCATTATGCTGAAAATGTTTCTATGTGG
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                                                                                                                                                                                                                                                                                                    AAGGCTGGCATGACCGTTAAGCAGGCTGTCCTTTATAATGCATTGTCAGCCATGCTGGCG
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/db_xref="taxon:9606"
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Best Local Similarity:
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  112
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Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 639)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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UI-M-FRO-cbe-c-22-0-UI.rl NIH BMAP FRO Mus
UI-M-FRO-cbe-c-22-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence: 132-213,
Seq primer: pYX-5.
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The following repetitive elements were found in this cDNA
The following repetitive elements were found in this cDNA
sequence: 132_213, >(TGG)n#Simple_repeat (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from Dr. M. Bento Soares, bento-soares@uiowa.edu
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
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SerAspHisGluHisHisSerAspHisHisProHisSerHisSerGlnArgTyrSerArg
                                                       ATCCACCACCATCACGACTACCAT----
                                                                                                         IlеНіяНівАярНівАярНіяНіяSerAярНівGluНіяНіяSerAярНіяGluArgHis 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP_FRO"
/clone_lib="NIH BMAP_FRO"
/clone_lib="NIH BMAP_FRO"
/note="Organ: Brain; Vector: pXX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Sonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to msNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
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KEYWORDS
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1 (bases 1 to 743)

pias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bordin,S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., Brunstein,A., Geoliveira, P.S., Bucher, P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI907176
AI907176.1
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RC-BT133-190399-076 BT133 Homo
                                                                                                                                             Bmail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=RC&t2=RC-BT133-076.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                              sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simpson, A.J.
                                                                                                                                                                                                                        Fax: +55-11-2707001
                                                                                                                                                                                                                                              Tel: +55-11-2704922
                                                                                                                                                                                                                                                               Brazil
                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl.
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                                                                                                            primer:
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
                                                                                          ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                        AlaValLeuLeuLysAlaGlyMetThrValLysGlnAlaValLeuTyrAsnAlaLeuSer
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eSerIlePheGluHisLysIleValPheArg 299
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                                                                  GTATTTCTTTTTACAAAAATGCTGGGATGCTTTTNGGGTTTTTGGGAATTATGTTACTTAT
                                                                                       yTyrPhePheLeuGln-AsnAlaGlyMetLeuLeuGlyPhe--GlyIleMetLeuIeuIl
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                                                                                                                                  TATGGNACCTGAAATGCTGCACAATGATGCCTAGTGACCATGGGATGTAGCCGTGGGGGG
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/clone lib="BT133"
/clone lib="BT133"
/clone lib="Common lib"
/mote="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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